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I, KIM MARSHALL, MANAGER EXAMINATION SUPPORT AND SALES,
hereby certify that the annexed is a true copy of the Provisional specification in
connection with Application No. PP 4963 for a patent by CSL LIMITED filed on
30 July 1998.

PRIORITY DOCUMENT

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day of January 1999

KIM MARSHALL
MANAGER EXAMINATION SUPPORT AND
SALES



AUSTRALIA

Patents Act 1990

CSL LIMITED

PROVISIONAL SPECIFICATION

Invention Title:

P. gingivalis polypeptides

The invention is described in the following statement:

specific amino acids. The microorganism has an absolute growth requirement for iron, preferentially in the form of haeme or its Fe(III) oxidation product haemin and when grown under conditions of excess haemin is highly virulent in experimental animals. A number of virulence factors have been implicated in the pathogenicity of *P. gingivalis* including the capsule, adhesins, cytotoxins and extracellular hydrolytic enzymes.

In order to develop an efficacious and safe vaccine to prevent *P. gingivalis* colonisation it is necessary to identify and produce antigens that are involved in virulence that have utility as immunogens to generate neutralising antibodies. Whilst it is possible to attempt to isolate antigens directly from cultures of *P. gingivalis* this is often difficult. For example as mentioned above, *P. gingivalis* is a strict anaerobe and can be difficult to isolate and grow. It is also known that, for a number of organisms, when cultured *in vitro* that many virulence genes are down regulated and the encoded proteins are no longer expressed. If conventional chemistry techniques were applied to purify vaccine candidates potentially important (protective) molecules may not be identified. With DNA sequencing, as the gene is present (but not transcribed) even when the organism is grown *in vitro* it can be identified, cloned and produced as a recombinant DNA protein. Similarly, a protective antigen or therapeutic target may be transiently expressed by the organism *in vitro* or produced in low levels making the identification of these molecules extremely difficult by conventional methods.

With serological identification of therapeutic targets one is limited to those responses which are detectable using standard methods such as Western Blotting or ELISA. The limitation here is the both the level of response that is generated by the animal or human and determining whether this response is protective, damaging or irrelevant. No such limitation is present with a sequencing approach to the identification of potential therapeutic or prophylactic targets.

In a first aspect the present invention consists in an isolated *P. gingivalis* nucleotide sequence, the nucleotide sequence consisting of or including a sequence selected from the group consisting of SEQ ID NO: 1 to 22, fragments thereof and sequences complementary thereto.

5 In a second aspect the present invention consists in an isolated *P. gingivalis* polypeptide, the polypeptide being at least partially encoded by a nucleotide consisting of or including a sequence selected from the group consisting of SEQ ID NO: 1 to 22, fragments thereof and sequences complementary thereto.

10 In a third aspect the present invention consists in an isolated *P. gingivalis* polypeptide consisting of or including an amino acid sequence selected from the group consisting of SEQ ID NO: 23 to 66 or fragments thereof.

15 In a fourth aspect the present invention consists in an isolated polynucleotide, the polynucleotide encoding a polypeptide consisting of or including an amino acid sequence selected from the group consisting of SEQ ID NO: 23 to 66 or fragments thereof.

20 In a fourth aspect the present invention consists in a nucleotide probe specific for *P. gingivalis*, the probe including a detectable label and a nucleotide sequence of at least 15 nucleotides, the nucleotide sequence being derived from a sequence selected from the group consisting SEQ ID NO: 1 to 22 and sequences complementary thereto.

25 In a fifth aspect the present invention consists in a composition for use in raising an immune response in an animal directed against *P. gingivalis* the composition including an acceptable carrier and/or adjuvant and at least one polypeptide having a sequence selected from the group consisting of SEQ ID NO: 23 to 66 or fragments thereof.

30 As will be understood by those skilled in the art the nucleotides of the present invention may be useful in DNA vaccination to reduce the incidence and/or severity of *P. gingivalis* infection.

plus insert DNA was blunt-ended with T4 DNA polymerase, then a final ligation to produce circular DNA was performed. Aliquots of Epicurian Coli Electroporation-Competent Cells (Stratagene) were transformed with the library DNA and plated out on SOB agar antibiotic diffusion plates
5 containing X-gal and incubated at 37°C overnight. Colonies with inserts appeared white and those without inserts (vector alone) appeared blue. Plates were stored at 4°C until the white clones were picked and expanded for the extraction of plasmid DNA for sequencing.

10 **DNA sequencing**

Plasmid DNA was prepared by picking bacterial colonies into 1.5ml of LB, TB or SOB broth supplemented with 50-100ug/ml Ampicillin in 96 deep well plates. Plasmid DNA was isolated using the QIAprep Spin or QIAprep 96 Turbo miniprep kits (QIAGEN GmbH, Germany). DNA was eluted into a
15 96 well gridded array and stored at -20C.

Sequencing reactions were performed using ABI PRISM Dye Terminator and ABI PRISM BIGDye Terminator Cycle Sequencing Ready Reaction kits with AmpliTaq DNA polymerase FS (PE Applied Biosystems, Foster City, CA) using the M13 Universal forward and reverse sequencing
20 primers. Sequence reactions were conducted on either a Perkin-Elmer GeneAmp 9700 (PE Applied Biosystems) or Hybaid PCR Express (Hybaid, UK) thermal cyclers. Sequencing reactions were analysed on ABI PRISM 377 DNA sequencers (PE Applied Biosystems). Raw trace data files from the ABI 377 sequencer were manually trimmed using Staden Pregap (Laboratory
25 of Molecular Biology, Medical Research Council, UK) running on a Sun Microsystem computer. Trimmed files were assembled into contigs using Staden Gap v4.1 and exported as FastA consensus files.

DNA sequence data was supplemented with sequence downloaded from the Internet site of the Institute for Genome Research
30 (<http://www.tigr.org>).

homology is present. Alternatively, protein coding regions may be identified using the ORF identification program GeneMark (3) using a matrix trained on published *P.gingivalis* sequences. This matrix may be further refined by adding ORFs identified from the results of homology searching and ORFs
5 identified by GeneMark. Otherwise, the program PSORT (4,6) may be used for the detection of signal sequences at the start of a protein and the prediction of cell localisation. A UNIX version of TopPred (5) may also be used to identify potential membrane spanning domains.

10 It will be appreciated by persons skilled in the art that numerous variations and/or modifications may be made to the invention as shown in the specific embodiments without departing from the spirit or scope of the invention as broadly described. The present embodiments are, therefore, to be considered in all respects as illustrative and not restrictive.

Dated this thirtieth day of July 1998

CSL LIMITED
Patent Attorneys for the Applicant:

F B RICE & CO

Table 1

SeqID#	Length of SeqID	Homology description	Length of homolog		% identity (aa)	Overlap (aa)	E value
			379aa	38			
1,23,45	337aa	NplD lipoprotein, <i>Haemophilus influenzae</i>	379aa	38	120	7.80E-09	
2,24,46	151aa	Hemolysin (TlyC), <i>Serpulina hyodysenteriae</i>	141aa	13	123	1.70E-07	
3,25,47	391aa	Major outer membrane protein, <i>Pseudomonas aeruginosa</i>	350aa	26	382	3.30E-07	
4,26,48	385aa	Major outer membrane protein, <i>Pseudomonas fluorescens</i>	317aa	29	233	2.20E-06	
5,27,49	190aa	Potential membrane protein, <i>Rhodobacter capsulatus</i>	193aa	46	190	6.80E-32	
6,28,50	833aa	Colicin I receptor, <i>Escherichia coli</i>	663aa	25	590	2.30E-10	
7,29,51	891aa	Protective surface antigen, <i>Helicobacter pylori</i>	916aa	20	825	1.90E-10	
8,30,52	170aa	Cationic outer membrane protein (ompH), <i>Yersinia enterocolitica</i>	164aa	27	168	4.40E-07	
9,31,53	163aa	Cationic outer membrane protein (ompH), <i>Yersinia enterocolitica</i>	164aa	23	160	5.70E-05	
10,32,54	827aa	Outer membrane protein (susC), <i>Bacteroides thetaiotaomicron</i>	1038aa	24	347	1.40E-06	
11,33,55	390aa	Heme receptor (hutA), <i>Vibrio cholerae</i>	693aa	24	368	6.80E-05	
12,34,56	462aa	Outer membrane protein (tolC), <i>Escherichia coli</i>	481aa	20	425	1.60E-09	
13,35,57	526aa	Neuraminidase, <i>Micromonospora viridifaciens</i>	647aa	32	375	2.10E-22	
14,36,58	245aa	Outer membrane protein (omp28), <i>Brucella melitensis</i>	250aa	24	178	0.0015	
15,37,59	276aa	Macrophage infectivity potentiator (mip), <i>Legionella israelensis</i>	242aa	35	219	8.80E-18	
16,38,60	775aa	Outer membrane protein (omp85), <i>Neisseria meningitidis</i>	792aa	21	699	0.0036	

Table 2 Results of protein analysis using Psort (6). Abbreviations used in the table are: OM = outer membrane, IM = inner membrane, PS = periplasmic space.
 * indicates an uncleavable signal sequence present.

Sed ID#	Signal present (Y/N)	Cleavage site	Cell location and probability		
			OM	IM	PS
67	Y	21	0.24	0	0.4
68	N	-	-	-	-
69	Y	20	0.62	0	0.13
70	Y	26	0.81	0	0.31
71	Y	13	0	0.5	0
72	Y	22	0.94	0	0.37
73	Y	40*	0	0.31	0
74	Y	20*	0	0.35	0
75	Y	18	0.21	0	0.93
76	Y	36	0.93	0	0.25
77	N	-	-	-	-
78	Y	27	0.25	0	0.54
79	N	-	-	-	-
80	Y	22*	0	0.38	0
81	Y	24	0.15	0	0.89
82	Y	23	0.79	0.7	0
83	Y	27	0.73	0	0.22
84	Y	24	0.94	0	0.38
85	Y	24	0	0.1	0
86	Y	18	0	0.12	0
87	Y	21	0.94	0	0.34
88	Y	25	0.2	0	0.61

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:
 5 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...477

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2

10	CCGAGCAAAA CGATAATTAA GACAATGGCA AAAATCAATT TCTATGCTGA AGGCAGTCAGC	60
	CTTCTCGGA TCAGAACGACG GATCGTCGGT AAGTGGATAG CCGAAGTATG CAGCCGATAT	120
	GGGAAAGCGG TGGGAGAAAT CTCTATCTT TTCTGTGATG ACGAATATAT CCTGAAAGCC	180
	AATCAGGAAT TTCTCGATCA TGACTACTAC ACCGACATCA TCACCTTCGA TTCCCTGCAGA	240
15	GCGGATACGG TGAATGGCGA CCTGCTTATC AGTCTCGATA CCCTACGCTC GAATGCCGT	300
	GCTCTTGATC TTCGATACGA AGACGAACGTG CATCGTGTCA TTATCCACGG CATACTGCAT	360
	CTTTGCGGAT TGAAAGACAA GAGCAAAAAG GATGAAGCCC AAATGCGTGC AGCCGAAGAG	420
	AAAGCCCTTG TCATGCTGCG AGAAACCATC GGATCGGAGC TTCCCTATT GCATACA	477

20 (2) INFORMATION FOR SEQ ID NO:3

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1185 base pairs
 (B) TYPE: nucleic acid
 25 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

30 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 35 (A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...1185

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3

	AAAAGTAAAA CTATGAAGGT AAAGTACTTA ATGCTCACAT TGGTTGGAGC AATTGCACTG	60
	AACGCAAGTG CACAGGAGAA TACTGTACCG GCAACGGGTC AGTTACCCGC TAAGAATGTT	120
45	GCTTTGCTC GCAATAAAGC AGGCAGCAAT TGGTTTGTAA CACTGCAAGG CGGTGTTGCA	180
	GCGCAGTTC TCAATGACAA CAACAACAAA GACCTCATGG ACCGCTTAGG AGCCATAGGT	240
	TCTCTTCTG TCGGAAAGTA TCACAGCCCT TTCTTGCAA CTCGTTTGCA AATTAACCGA	300
	GGTCAAGCCC ACACCTTCCCT CGGAAAAAAAT GGCAGAACAG AAATCAACAC CAATTGTTGGT	360
	GCAGCTCACT TCGACTTTAT GTTGATGTG GTTAACTACT TTGCAACATA TCGCGAAAAT	420
50	CGTTTCTTCC ATTAAATTCC ATGGGTAGGT GTTGGCTTAC AACACAAATT CATCGGTAGC	480
	GAATGGAGCA AAGACAATGT GGAATCACTG ACGGCGAATG TAGGAGTTAT GATGGCTTTC	540
	AGATTAGGAA AGCGAGTAGA CTTTGTGATC GAAGCACAAG CAGCTCACTC CAATCTCAAT	600
	CTAAGTCGCG CATAACAATGC CAAGAAAAACT CCCGTATTG AAGATCCCGC AGGACGTTAT	660
	TACAATGGAT TCCAGGGGAT GGCTACAGCA GGTCTTAATT TCCGGCTGGG AGCCGTAGGC	720
55	TTCAATGCCA TTGANCCAAT GGACTACGCA CTTATCAATG ATCTGAATGG TCAGATTAAC	780
	CGTTTGCAGCA GCGAGGTCGA AGAACTCTCA AAACGTCCTG TATCATGCC CGAATGTCCT	840
	GAAGTAACTC CTGTTACTAA GACAGAAAAAT ATACTGACGG AAAAAGCTGT ACTGTTCCGT	900
	TTCGACAGCC ACGTTGTGGA CAAAGATCAA TTGATCAACC TGATGACGT AGCTCAGTTT	960
	GTAAAAGAAA CTAACGAGCC GATTACCGTT GTTGGTTATG CTGATCCTAC GGGTAATACT	1020
60	CAATACAACG AGAAATTGTC TGAGCGTCGG GCTAAAGCCG TTGTTGATGT TCTGACAGGT	1080

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 5 (A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:
 (A) NAME/KEY: misc feature
 (B) LOCATION 1...585
 10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5

GTAATTGGCA	TCATTATGGA	ATTTTCATG	TTATTCTAG	CGGCGGTTT	CGTTAATAAC	60
GTCGTGCTGT	CGCAGTTCT	CGGTATATGC	CCATTCTTAG	GCGTATCGAA	GAAGGTAGAC	120
15 ACCTCAATCG	GTATGGGTGC	AGCCGTGACA	TTCGTATTGG	CACTGGCTAC	CTTGGTTACC	180
TTCCCTGATTC	AGAAGTTCGT	TTGGATCGT	TTCGGATTGG	GCTTTATGCA	GACCATTGCA	240
TTTATTTTGG	TCATTGCCGC	CTTGGTGCAG	ATGGTGGAGA	TCATACTCAA	GAAAGTATCT	300
CCTCCCCTCT	ATCAGGCACT	GGGTGTATTTC	TTGCCCTTG	TTACGACGAA	CTGCTGTGTG	360
20 CTCGGTGTGG	CTATTTGGT	TATCCAGAAG	GATTATACCC	TGCTCCAGAG	CTTCGTCTAT	420
GCAATATCCA	CGGCTATCGG	TTTCACCTTG	GCAATGGTTA	CTTCGCAGG	TATTCGAGAG	480
CAACTCGATA	TGACCAATCT	CCCCAAAGCT	ATGAAGGGAA	TACCTTCGGC	ACTCTGGCT	540
GCGGTATAT	TGGCTATGGC	TTTCATGGC	TTCAGCGGT	TCGCC		585

25 (2) INFORMATION FOR SEQ ID NO:6

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2628 base pairs
 (B) TYPE: nucleic acid
 30 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

35 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 40 (A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:
 (A) NAME/KEY: misc feature
 (B) LOCATION 1...2628
 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6

TACCGATCTT	ATCGTGGGAT	AGGGAGTGGG	ACACACTCTC	CTAACCTCAA	AAACCGACTA	60
AAAAGGATCG	GAATAAGGAT	ACCGAACAGA	CACTATATCC	ATATCAAGCC	AATCAAACCA	120
50 AAAAATAAAA	TGAAACAAC	AAACATTATC	AGCTTCATCA	TTGCTTCC	ATTCTTAGGA	180
ACGAGCGCAT	CGGCTCAGCA	ATCAGGGCGGA	TCCGTTACAG	GTACCGTAGT	GGACAAAAGC	240
TCAAAAGAAC	CTATCGCATA	CGTACAAGTA	TTCGTCAAAG	GAACCACTCT	CGGAACCTCC	300
ACGGATGCAA	ACGGAAACTA	CTCGATCAAG	GGAACTCCTT	CGGGTAATCA	AACTATCGTA	360
GCCCAGCTCA	TGGGTTACTC	CACTTGCAGA	AAAAAAGTAC	ATATAGAAAA	GGGTGGTTCC	420
55 CGCCACGTAG	ACCTCTATCT	GACCGAAGAG	ATTCTCTCTC	TCGATGGGGT	AGTGGTATCT	480
GCCAATAGAA	ACGAGACTTT	CCGCCGTCAA	GCACCCCTCGT	TGGTAACGGT	ACTGTCGCCG	540
GAACTTTCC	TCAAAACCAA	CTCTACCAAC	CTGAGTCAGG	GACTTAAGTT	CCAGCCCGGT	600
CTGCGCGTGG	AGGACAACGT	TCAGAACTGC	GGTTCAACC	AAGTCGTAT	CAATGGACTC	660
60 GAAGGAGCCT	ATTGCGAAAT	TCTTATCGAC	AGCCATCCCA	TCTTCAGTTC	GCTTGGCGGT	720
GTCTATGGCT	TGGAGCAGAT	GCCTGCCAAT	ATGATCGAAC	GTGTAGAAGT	AATTGCGGGT	780

	GATGAAGTCC	TGATTCCCTGG	AGATGCCATG	TCTGCTGCCG	TGAATAGAAT	TATGCGTCAG	300
	GGCTACTTCT	CAAATGTGCG	AATCATCGCG	GATAAAATATG	TCGGCAATAA	AGTCTATCTG	360
	AAAATCATTG	TCACTGAACG	TCCTCGCATC	AGTAAGGTTA	CTTTAGCGG	GGTAAAGAAG	420
	TCTGAGAGAG	AAGATCTTGA	AATGAAAATC	GGTCTTCGCG	AGGGGATTCA	GATGACCAGA	480
5	AATAATGAAG	ACAAGGTCA	GCAAATCGTA	CAGAAGTATT	TTAGTGAGAA	AGGTTATCGC	540
	GATGCCAGCA	TACGGATAAC	GCAGGAACCG	GATCTTCCA	AAGATGGCTT	TGTCAATGTG	600
	CTTATCTCGA	TTGAGAAGAA	AAGCAAAACC	AAGGTGAATG	AAATTTATT	TTCCGGCAAC	660
	AAGGCCCTA	GCAATCATAA	GCTAAGAATG	GCGATGAAGA	ACACCAATGC	CAAATCAGT	720
	CTTAGAAAGC	ATATTCGCTC	ATCTTCTTG	AAACTTTTA	GTACTCATAA	TTTGATGGAA	780
10	GAGAGCTACC	GTGAAGATT	GGTCGATTG	ATAGAGAAGT	ATCAGGAAT	TGGATATCGT	840
	GATGCTGAA	TACTGACCGA	CAGTGTCTG	AAGGCTCTG	ACGGCAAAG	AGTGGATATT	900
	TATCTCAACA	TCGAAGAGGG	GCAGAAGTAT	TATATTAAAGG	ATGTCAACTT	TGTGGGCAAT	960
	TCACAATATC	CATCGGAGTA	TTTGAACGA	GTGCTCGGAA	AAAATCCGG	AGATGTGTAC	1020
	AATCAGAGAC	GATTGGCTAA	GCGCTCAAT	GAAGATGAAG	ATGCTGTGGG	GAACCTGTAC	1080
15	TATAAACATG	GCTATATTT	TGCGTGGGT	GATCCCCTGG	AAACAAATGT	AGTGGGGGAT	1140
	TCTGTTTCG	TTGATATTG	TATAGCGGAG	GGGAAGCAGG	CCAATATCAA	TAAGGTGATC	1200
	ATCAAAGGAA	ATACTGTCGT	GTACGAAGAC	GTAGTACGCC	GAGAGTTTA	CACAAAGCCC	1260
	GGCCAGCTCT	TTAGTCGCGA	GGATATCATT	AACTCTATT	GTCTCATCAA	TCAGCTTGGG	1320
	CATTCGATG	CCGAAAATC	TATCCCCGT	CCGATTCCCA	ATCCCAGAAC	AGGAACAGTG	1380
20	GATATAGAGT	ATGATTTGGT	GCCGCGTAGC	AGTGACCAAT	TGGAGCTTC	TGTCGGTTGG	1440
	AGTCAGTCCG	GACTTCTGTT	CCGAGGAGCC	ATTAAGTTCA	CGAACCTCTC	TGTCGGCAAC	1500
	TTGCTCCATC	CCTCGATGTA	TAAGAAAGGG	ATCATTCCGC	AAGGGGATGG	GAAACACACTA	1560
	TCACTGAGTG	CTCAGACCAA	TGGAAAGTAC	TATCAGCAGT	ATAGTGTAC	ATTATGGAT	1620
	CCATGGTTG	GGGGCAAGCG	GCCGGATATG	TTCAGCTCA	GTGCATTCTA	TTCCAAGACT	1680
25	ACGGCGATTG	ACTCCAAGTT	CTACAATAGC	AATGCCGGCA	ACTACTATAA	TGCCTACTAT	1740
	AATAGCTACT	ACAACAACTA	TAATAGTTAT	TACAACGGTA	TGTCGAACTA	TACCGCGAC	1800
	CTCTATACTC	AGGCCAGCGA	TCCGGATCGT	TCGCTTCAGA	TGTTAGGTAC	TTCGATCGGT	1860
	TACGTAAGC	GTTTGACTTG	GCCGGACAAT	TGGTTCCAGA	TTTATACTTC	TCTGAACACTAC	1920
	ACCTACTATA	GACTGCGAAA	TTGGAGCTAC	AATAACCTCC	AAAATTTCCA	TCATGGCTCG	1980
30	GCTAATGATC	TCAACTTGG	GCTGCGTCTC	TCTCGTACTT	CCATCGATAA	TCCTATTTAT	2040
	ACCAGAACGCG	GATCGGATT	CATGGTTCT	GTTGCTGCTA	CTCTTCCTTA	TTCTTGTGG	2100
	GACAATCATG	ACTATGCCAG	CCAGAACCTC	AGCGTAAGCG	ATCGTTACAG	ATTATATCGAG	2160
	TATCACAAAGT	GGAAGTTTAG	AGGACGAGTT	TTTACTCCAT	TGCTCAATCC	TGCTACGCAT	2220
	AAATATACAC	CGGTGCTCAT	GAGTCGAGTG	GAAGGAGCAG	TTCTTGGTT	GTATAATTCC	2280
35	AATAAGAAAT	CTCCTTCCG	TACTTCTAT	ATGGGAGGTG	ATGGTATGTC	CAGCTATTAT	2340
	GGTGGCTACA	TGAATGAGAC	TATAGGTTTG	CGTGGTTATA	AGAACGGATC	TATTGCCGGT	2400
	AATAACGACT	ACTATGCA	TGCTTATATG	CGGCTTACGA	TGGAACACTAC	TTTCCCGATT	2460
	CTGTTTGGAAA	ACTCATTCAA	TGCGTGGCTC	TTAGCTTTG	CCGAAGCAGG	CAATGCGTGG	2520
	CGCAGTATCG	ACAATTATAA	TCCCTTAAC	CTGAAGCGAT	CGGCCGGTGT	AGGATTGCGT	2580
40	GTAACGTTAC	CGATGGTCGG	AATGCTCGGT	ATCGATTGGG	GATATGGCTT	TGACCGTCCG	2640
	GACAATTCTC	TACAGCGAGG	AGGAAGCAAT	GTCCACTTTG	TGCTCGGACA	GGAGTTC	2697

(2) INFORMATION FOR SEQ ID NO:8

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 531 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

50 (ii) MOLECULE TYPE: DNA (genomic)

55 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Porphyromonas gingivalis*

60

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...531

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8

CAAATAAAACA	TGAATGGCGA	TATGAAACGG	TTTTGATT	TGATCGGCCTT	TGCACGGCG	60
GTAGCTTCT	CCGGTTTTTC	CCAAAAGTTC	GCTTTGGTAG	ATATGGAATA	TATCCTCAGG	120
AATATTCCTG	ACTATGAGAT	GATGAACGAA	CAGCTGGAAC	AGGTGTCAA	GAAATGGCAA	180
10 AATGAAATCG	AAGCTCTCGA	AAATGAAGCC	CAATCTATGT	ATAAGAAGTA	TCAGAGCGAT	240
	CTCGTATTCT	TGTCTGCTGC	ACAGAAGAAA	ACCCAAGAAG	AGGCTATCGT	300
	CAGCAAGCAT	CCGAGCTCAA	GCGGAAGTAT	TTCGGCCCGG	AGGGGGAGCT	360
	CGCTCCGATC	TGATGAAGCC	TATTCAGGAT	GAGATTGGA	GTATAAGAAA	420
15	AAGCGTAACA	ACTATCAGAT	GGTGCTTGAT	AGAGGTACGT	CCGGAATTAT	480
	CCGTCTATTG	ACATTAGCGA	CCTTGTACTG	AGCAAGATGG	CTTTGCCAGT	531

(2) INFORMATION FOR SEQ ID NO:9

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 510 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

25 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

30 (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis

35 (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...510

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9

CGAATAAAATA	AACAACACGA	AATGAAGAAA	TTTTTCTCA	TGCTTCTGAT	GGCTCTTCCT	60
TTGAGCCTCT	TGGCACAAAA	GGTGGCAGTG	GTAAACACTG	AGGAGATCAT	TTCCAAAATG	120
CCGGAACAAG	TAGCTGCTAC	AAACACAGCTC	AACGAATTGG	CCGAAAAGTA	TCGCCTTGAT	180
45 CTCAGAGTA	TGGACGATGA	GTGGCCAAA	AAGACAGAAG	AATTGTAAA	GGAAAAAGAC	240
TCTCTACTGG	AGAACATCCG	CAATCGTCGT	CAGCAGGAAC	TTCAGGATAT	TCAAACCTCGT	300
TATCAGCAGT	CATACCAAAAC	GATGCAGGAG	GATTTGCAA	ACCGCCAACA	ACAGCTTTT	360
GCTCCTATCC	ACACAAAGGT	GGCTGATGCC	ATCAAGAAAG	TGGGTGACGA	AGAAAAGTGT	420
GCCTACATCA	TGGAGGCCGG	TATGATGCTT	TACACCGGAG	CTACTGCTAT	TGACTTGACC	480
50 GCAAAGGTAA	AAGCGAAACT	CGGAATCAAG				510

(2) INFORMATION FOR SEQ ID NO:10

55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2484 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

60 (ii) MOLECULE TYPE: DNA (genomic)

5

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1191 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- 10
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 15
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Porphyromonas gingivalis*
- 20
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1191

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11

AGAAATCGGA	GAACATAAAC	AATGCCGATC	CCACCGGTTT	CATCAACTAC	AAAAGCGACT	60	
ACTACACCTA	TGGTGCCTTA	CTCCAGGACA	AGATTTCTT	TGGAGGACAA	AAATATCGTA	120	
CTCGGTGTCG	ACAGCCGAAA	CATGACGATG	GAGTCAGAAA	GATTGAGCA	GGCAGGAGTG	180	
25	AATACAAAGC	CATACAACCC	CGGATATGCC	ACGAACAATA	TCGGTTTGT	CGGACAGGCC	240
AATTCTTCTACC	TGCTGAACGA	TGCTCTATCG	ATATCTGCG	GTGCACGTGC	CGACTTCATG	300	
TTCTTTGACC	TGAAAGCGAA	CGAGTATCTC	AACAATGAAG	CCAAACAGGA	AACTCATAAC	360	
GTAATCAATC	CGAATGTCGG	AATCAAATAT	GAGTTTGTGA	AAGGCCTTAC	AGCTCATGGT	420	
30	ACATTGGTA	GTGCATTCAAG	TGCTCCCGAT	GCTTCCAAA	AAGCAGGCCA	ATACGTAGGC	480
CCGTTGGCA	CGACCATAGG	CAATCCTGAC	CTGAAACCCG	AAAAGTCCAT	GACCTGGGAC	540	
TTCGGTATCG	GATACAGCAA	TGCACGCTGC	GGGATCCAAG	CCGACGTAAC	CTTAACCTAT	600	
TTCCACACCG	ACCACAAAGA	TCTGATCTTG	TCCAGCCCTG	ACTATGCTAA	TAATATCACC	660	
ACATACATCA	ATGCCGACAA	GGCTCGTATG	AGCGGTATCG	AGGCCCTTT	GTCTTATGAC	720	
35	TTCGGCAGCC	TCTTTGCCAA	CAAGTTCTCT	CTCCGGCAT	TTGCGAATGC	CACGATCATG	780
CTCAATTCCG	AGATGAAGAA	AAGCCAGACC	GATGCCCTT	GGAGCGAAAT	GTACTACGTT	840	
CGCAAGCAGA	ACATCACCTT	CGGTATCGAA	TATCGTGGCA	AAGAAGGACT	TGAAGTGATG	900	
CTCAACGGTC	GCTTCATGGG	ACGCAGGATC	GAGCAAACACT	GGTATGCTTA	CTACCCGAA	960	
GTTCGCCCCG	AACTCCAGCA	ACTGCTTGCA	GCAGAAGAGC	CTGAATTGGC	TGCTCAGGGA	1020	
40	CTGCTCCGTC	ATCCGCAAGC	AATGGTGTTC	AATGCCCTCG	CTTACTACCA	CATGAACAAG	1080
TATCTCACCT	TCGGTGTGAA	CTTGAACAC	ATCTTGATG	AGCTTTATAC	GGAGAAAAGAC	1140	
GGCTTACACCA	TGCCCCGGACG	TAACATCATG	GGTAAGGTTA	TGGTCAACTT	C	1191	

45 (2) INFORMATION FOR SEQ ID NO:12

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1452 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

50 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

55 (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Porphyromonas gingivalis*

60

	ATTCGTATCG	GATTCTCTCT	TCCGAAAGAA	ACGGAGGAAA	AAGTCACCGC	CCTATATCTC	300
	CTTGTGAGTG	ATTCTTAGC	GGTGCACGAC	TTGCCGACT	ACAAAGGGCG	AGTCTCTTAC	360
	GATAGCTTCC	CGATCTCAA	GGAAAGATCGT	ACCACAGCCC	TTTCTGCAGGA	TTCGGTAGCC	420
	GGACGCCGCT	TCTTTTATTT	GGCTGCAGGAT	ATAGGGCTG	TTGCTTCTTT	TTCCCGATCC	480
5	GATACTGTA	CTGCCGCTGT	GGAAAGAGGTG	GCTGTCGATG	GCCGCCCTT	GCCGTTGAAA	540
	GAGCTGTCGC	CTGCCTCCCG	TCGTCGTAT	AGGGGGTATG	AGGCCCTCTT	TGTACCCGGT	600
	GATGGCGGAT	CGCGGAACTA	TCGTTACCCG	GCCATTGAA	AAACGGCTAA	TGGAACACTC	660
	ATAGCGATGG	CCGACAGACG	AAAATATAAT	CAGACGGATC	TGCCGGAGGA	TATAGATATA	720
	GTCATGCGGC	GCAGTACCGA	CGGAGGGAAA	TCGTGGAGCG	ATCCCAGGAT	TATCGTACAG	780
10	GGAGAGGGGC	GCAATCATGG	CTTGGCGAT	GTAGCCCTGG	TGCAAACCCA	AGCAGGAAAG	840
	CTCCTGATGA	TCTTGTGCG	TGGAGTAGGC	CTGTGGCAGT	CTACCCCCGA	TCGTCCCTCAG	900
	CGCACTTATA	TATCGGAAAG	TCGGGACGAA	GGACTGACTT	GGTCGCCTCC	TCGGGATATA	960
	ACCCATTCTA	TCTTCGGCAA	GGATTGTGCC	GATCCGGGAC	GCAGTCGCTG	TGTGGCCTCC	1020
	TTTGTGCTT	CGGGACAAGG	GCTTGTGCTG	CCATCCGGTC	GTATCACGTT	TGTGGCTGCC	1080
15	ATCCCGAAT	CAGGGCAGGA	GTACGTCCTG	AACAACATG	TCCCTATAG	CGACGATGAG	1140
	GGCGATACAT	GGCAGCTTC	CGACTGTGCA	TACCGCCGTG	GCGATGAGGC	AAAGCTTCA	1200
	TTGATGCCCG	ATGGCAGGGT	ACTGATGAGC	ATACGCAATC	AGGGACGGCA	GGAGAGGCCGA	1260
	CAGCGTTCT	TCGCTCTCTC	CTCCGACGAT	GGCCTTACTT	GGGAGAGAGC	CAAGCAGTTC	1320
	GAGGGCATCC	ATGACCCCGG	CTGTAATGGA	GCTATGCTTC	AAAGTAAAAAG	GAACGGAAGG	1380
20	GATCAAGTGC	TGCACTCCCT	GCCTCTCGGC	CCGGATGGGC	GTCGCATGG	AGCTGTCTAT	1440
	CTCTTCGATC	ATGTCTCCGG	CCGCTGGTCC	GCTCCCCTTG	TTGTCAATT	AGGATCGAGT	1500
	GCCTACTCGG	ATATGACTCT	GCTGGCGGAT	GGAACGATCG	GTTATTCGTT	CGAAGAGGGC	1560
	GATGAGATCT	CATTGGTTTT	CATTGGTTC	GTCCTTGACG	ATCTCTCGA	TGTCCGGCAA	
25	1620						

(2) INFORMATION FOR SEQ ID NO:14

	(i) SEQUENCE CHARACTERISTICS:						
30	(A) LENGTH: 879 base pairs						
	(B) TYPE: nucleic acid						
	(C) STRANDEDNESS: double						
	(D) TOPOLOGY: circular						
35	(ii) MOLECULE TYPE: DNA (genomic)						
	(iii) HYPOTHETICAL: NO						
40	(iv) ANTI-SENSE: NO						
	(vi) ORIGINAL SOURCE:						
	(A) ORGANISM: <i>Porphyromonas gingivalis</i>						
45	(ix) FEATURE:						
	(A) NAME/KEY: misc_feature						
	(B) LOCATION 1...879						
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14						
50	AAGTCTCCGA	GCGATTCCGGC	TTTGGCGTCG	GTATGGAGCG	CGAACATAAT	ATCTGGACTC	60
	GTGGTGGGAA	AAACGATTAC	TTTGCTTATC	CTGTATTCTA	TGGCGATAAG	AAAGTAGTAAT	120
	ATAGAATCAA	TACAGTGCCTT	TGTGATGAAA	AAAGAAAAAC	TTTGGATTGC	GATCGTCGCC	180
	GGTTTGGCTT	TCGTATTGGG	CCTTATGCT	CTTGGCGCGA	GTGTCGCTCA	GCTACGCCGC	240
55	TCTCAGCCTT	CGGTGACTGT	GACCGGTATG	GCCGAGCGTA	ATTCAAATC	CGATCTGATC	300
	GTTTGGACTG	CTTCGTACCA	GCTCCAGATG	ATGGATCTCG	AATCGGCCTA	CAAGGCTTTG	360
	AAGGAAAAAC	AGATATTGGT	AGCAGACTAT	TTGAAAAACA	AGCAGCTGCC	CGATTCGTCT	420
	TATATCTTCT	CAAGCGTAGC	CATCTCTAAA	GAATACAAT	ACTATTACGA	TCCTCGGCAG	480
	GAACAAAACG	TCAGGACCTT	TGCCGGGTAT	CTGCTCAGCC	AGACAGTTAC	GGTGACCTCA	540
60	CAGGACATCG	AACATGTGGA	AAAAATATCT	CGCGATATAA	CGGAGCTGAT	CAATCAGGGG	600
	GTAGAGATTA	CCTCCGACCG	TCCGGCCTAT	TACTACACCA	AGCTCAATGA	TCTGAAGGTG	660

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:
 5 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...2409

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16

10	TGTGAAAGC AGAACGCTCTC AAACCCGAAG AGGAGCCGGT ATCCGTGCAG ACGGATATCA	60
	TTCCGACAAA GCGATAAGAA TCCGATGAAA GTATTACGGC AAGTATTCCCT CCCCCATCCTT	120
	TTTGTCTAC TGACAGGTGC CTGCTCCACC ACAAAAGAATC TGCCGGAAGG CGAACAGCTG	180
	TATATCGGAA TGGGCAAGAC ACAGATACTC CGGCAGGACA AGAGCCACGC CGGCCAACAG	240
	GCTCTGACCG AAGTGGAGAG TACACTGAAA GTTACACCCA ATGGAGCTAT TTTGGCAGT	300
15	GCAAGTGCCT CCTTACCCAA GATACCATTC GGGCTATGGC TATACAAACAG CTTCGTGGGG	360
	GATTCCTACTG TCATTTGAA ATGGATATTG GACAAGTTG CAGCCAAGGCC GGTTTCATC	420
	AGTCAGGTCA AATCCGATAG CCGGGCTAAG GTGGCGACGA ACATCCTCCG CGAACACGGG	480
	TACTTCGATG CTAAAGTAA AAGCAGTGTG ACCACTCTGA AAAAGGACTC GCTCAAAGCC	540
	AAAATCTCCT ATACGGTGGA TATGGCCTCT CTTTATCATT ACGACAGCAT CATTCCCTTA	600
20	CCGATCAGCA CTTTCCCCGA CAGCATTCTG GCTTACAGGC AGACTCCGTC TTTGATCAGG	660
	AAAGGAGACC AGTTCAATTG GGCAAAGCTG CACGAAGAGC GTCAGACCAT CAGTCCCTG	720
	CTGAGAGACA ATGGTTACTA CTACTTCCGC CCACAGGATA TTATCTACGA AGCCGATACC	780
	CTCCTCGTAA GAGGTGCCGT ATGCCTGCAG GCCAAGCTCT CGGAAGATAC TCCACCCCAA	840
	GCCATGCGCC CGTGGAGGAT AGGGAAACGG ACAGCAGTCC TGCTCGGAAT GAACGGAGAA	900
25	AGCCCGACAG ACTCGCTCGA AGTGGAGGAT ATGAAAGTCC TTTACTATCG TAAAATGCCG	960
	GTTCGCCCCA AGATTTGGC CAAACGCTTT CGTTTCTTCT CCGGCAATCT GTATCGGCAG	1020
	AAAGACGATG AGACGACACG CAAATCCTTG GTCGTTTG GAGCCTTCTC CGTTATCGAT	1080
	CTCAATTGTT TGCAACGCGA TTCCATTTCG GGCCTTTGG ATGTGCGACT GCTAACCAACC	1140
	CTCGACAAAC CTTGGGATGC ATCATTAGAG ACCTTGTCA CGAGCAAAAG CAATGACTTC	1200
30	ATCGGTCCCG GACTGAATT TGCTCTTGT CGGGCGCAATG TATTGCGGG AGGAGAAAAT	1260
	CTTTCTTGGG ATATCGGTGG ATCGTATGAG TGGGAGACCG GCAATCGTCC CGAAAATAGC	1320
	AGCAATCGGC TGATCGATAT AAAATCGTAC AACATGAAATA CGGCCGTGAA CCTCTCGTTT	1380
	CCCTCGATTG TATTCGGGG TCTGCTGGAT AAATACTATT ACTACCCAC GACTACGACT	1440
	TTTCAGGCTT CTGCCACCGC GCTGAACAGG GCACACTACT TTAGCATGTA CTCTTCGGC	1500
35	TTTCGACCA CCTACGAATT TCAGCCCTCC AAGGAACACC GGCATGCTAT TTTCCCGCTC	1560
	AAGCTCAACT ACAACCTCCT GGGGCATCAG ACAGAAACTT TCCAGGCCAT TACGGCGAAC	1620
	AATCCGCCCC TGCTGCTCAG CCTTCAGAGT CAGTTCTTG CTCAAATGGG GTATATCTAT	1680
	ACGTTCAACA AATCCGTTTC AGAGAAAAGT CCTCATCATC TTGGGATGCA ATTGGACTA	1740
	TCCGAGGCA GCAATCTCCT GAATCTGATC TATCTGGCAG CCGGCAAGAA GTACAGCGAC	1800
40	ACCAAGAATT TCGTCGGCGT CCCCTTCTCT CAGTTCATCA AAGCCACGGG AGAACTGCGC	1860
	TATTCTATA CCATAGACCG CAATCAGTC CAATCAGTC CTGGCAACCC GTTCGGGAC AGGCGTGATA	1920
	TATAGCTATG GCAATATGCG AGTGGCACCC TATAGCGAGC AGTTCTATGT AGGCGGTGCC	1980
	AATAGTATCA GAGCTTCAC CGTCCGTAGC ATCGGCCCCG GACGGTTCAA TCCGGATTCC	2040
	GACAATCAGT ATTCTATTT GGATCAGGTG GGCAGATTCA AACTCGAAGC CAACGTGGAA	2100
45	TATAGAGGCA AGCTTTTCGG GGATCTCCAC GCAGCCGTT TCCTCGATGC GGGCAACGTT	2160
	TGGCTCTTGA GGGAGGATTC TTCCCCTCCG GGCCTGCTC TGCCGAAGT GGGATCGGTG	2220
	AGCAATTTCG TGAATAGCAT CGCTCTCGGC ACCGGTGTG GCCTCGCTA CGATCTGGCA	2280
	TTTCTCGTGG TTCGTGTCGA TGTCGGCTTC GGTCTCCACC TTCCCTAACAA TACGGGTAAG	2340
	AAAGGTTACT ACAATATCCC ACGCTTAAAG GATGCCATCG GTTCCATTG GGCTGTCGGC	2400
50	TATCCCTTC	2409

(2) INFORMATION FOR SEQ ID NO:17

55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2349 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

- (A) LENGTH: 2625 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

5

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

10

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

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(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...2625

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18

GTGGAATCTA	AATTGTTATG	TCTTATGAGA	AAAAGAAATTTC	TACAACCTTT	CCTGACCGCA	60	
TTGCTGCTGG	CATTAGGCTC	CTCTCTCGCC	ATAGCGCAAA	CAGTGGTGAC	CGGTAAGGTG	120	
ATCGATTCAAG	AAACGTCCGA	ACCGCTCATC	GGTGTATCCG	TAAGCACCGG	TCAGGGAGCA	180	
TCCCTCCGCG	GTGTAACCAC	CGATATGGAT	GGTGGCTTCC	GATTGAAAGT	ACCGGCCAAA	240	
TCTGTCTTGA	CTTTCGTTG	CGTAGGTTAT	GCTACCGTAA	CTCGCTCTAT	AGGCAGAGGT	300	
TCTCAAGAAG	ACCTCGGTAC	GATTCTCCTC	GATCCCCAGG	CCATCGGCTT	GGATGAGATT	360	
CAGGTAAATAG	CCTCTGTGGT	GCCCAAAGAC	CGTATGACGC	CGGTACCCGT	TTCCAATATC	420	
CGTGTGGCTG	ATATTCAAGC	AGCATCGTTG	AATGTCGAAT	TTCCCGAACT	GGTTAAATCC	480	
ACTCCCCTCTA	CCTATACGAC	AAAAGGAAGC	GGAGGTTTCG	GTGATGGTCG	TACCAATGTG	540	
CGTGGATTTCG	ACACTTACAA	CTTCGGTGTG	CTCATCAACG	GAGTCCCTGT	CAATGGTATG	600	
GAAGACGGGA	AAGTATATTG	GAGCAATTGG	AGTGGTCTGA	TGAATCAAGC	CAGTACCAATT	660	
CAGATTCAAGC	GCAGACTCGG	AGCCTCCAAG	CTCGGTATCA	GCTCGTAGG	TGGTACGATG	720	
AACATTATCA	CGAAGACTAC	GGACGCCAAC	ACCGGAGGTT	CGGTTATGGT	CGGTATGGGT	780	
AATGATGGAT	TGCAACAAAGA	ATCGTTCTCC	ATTCTACGG	GTATGAAACG	CGGTTGGGCT	840	
ATCACCAATTG	CAGGCTCCCC	TATGACGGGT	CTGGGTTATG	TGAAGGGGCT	GAAGGGACGT	900	
GCATTCTCTT	ACTTCTTCAA	CGTTTCGAAG	AAGTTCAATG	AACGTCATAC	CCTCTCTCTT	960	
ACCGGATTCTG	GTGCACCACA	ATGGCACAAAC	CAACGTTCTT	CCAAATATTC	TGTAGCCGAC	1020	
TATGACAAAT	ACGGCATCCG	TCACAATCAA	TCCTTCGGCT	ATCTGCGAGG	CGAACTGACT	1080	
CCTACGGCTT	ATGCTTACAA	TACGTACAC	AAGCCCCAGT	TCTCGCTGAA	CCACTCTCTGG	1140	
AAGATGGATG	AAAATACCTC	TCTTATACG	gCANCCTACG	CATCTTGGC	TACCGGTGGA	1200	
GGTCGTCGCG	CTTATGGAAA	GAACAGTAAG	TGGGTATTGA	TCAACTACAA	CACCGGACAA	1260	
CCCTATGAAC	AAACAAAGGT	GACTCCGAT	GGACTTATCG	ACTACGATGC	CGTACTGGCT	1320	
GCCAATGCTG	CGGCGAGCAA	TGGCTCGGAA	GCAATTTCG	CCCTTGGCTC	CAACTCTCAC	1380	
AAGTGGTCG	GTCTACTCTC	TTCATCAAG	AAGAAACTTA	ATAGTCGCT	GAACCTTGACA	1440	
GCCGGATAACG	ATGGGCGTTA	CTACCGTGGC	GACCACTATG	ACAAGATCAC	CGATCTGCTC	1500	
GGCGGTAGCT	ACTACATAGA	GGATCCAAG	ACAAAGCTCG	CATACCATGC	GGAAAGTCAG	1560	
CAACTGAAAG	TGGGTGACAT	TGTAAATCGG	GACTACACAG	GCGAAATCAT	GTGGCACCGC	1620	
CTCTTCGCAC	AGATGGAGCA	TTCGTCGCAA	TGGATCGATG	CATTGTCATC	AGGATCTATC	1680	
AACTACGAAC	TATACCGCAA	TCACAACTAT	GGCGGTAGCA	AGTCACCCGG	CTACCTGCC	1740	
GGCGTATCGC	CGTGGAAAG	CTTCCTTCG	TGGAGTGGCA	AGGCAGGTCT	GAGCTACAAG	1800	
TTCGCACAGG	GACACAATGT	ATTCCGCAAT	GGCGGTTCT	TCACACGTGC	ACCAACTCTT	1860	
GGCAATATCT	ATGCTGCGGG	GGCTATCATT	CCCAATGACA	AAGCCAATAT	GGAAAAGGTG	1920	
CTTACAGGAG	AGGTCGGCTA	TGGATTACAG	AATCACAAA	ACTTCGAGTT	CAATATCAAC	1980	
GGATACTATA	CGAAGTGGAT	GGATCGCGTG	ACCTCGAAGA	GAATCGGAAA	CGAGTATGTT	2040	
TATCTCAATG	CGCTTGATGC	TGTTCACTGT	GGGGTAGAGG	CTGAGGTCAG	CTATCGTCT	2100	
ATTCGTCAGA	TCGACCTTCG	CGGTATGTT	TCTCTCGGTG	ACTGGACTTG	GCAAAACAAT	2160	
GTAAGTTACA	CTTCTTACGA	CGAAGCCGGC	AATGAGACAG	GGCAGGATAT	AACCTATATC	2220	
AAGGGTCTTC	ACGTCGGAGA	TGCAGCACAG	ATGACGGCTG	CTGTATCGGC	AGACATAGAG	2280	
CTGTTCAAGG	GTTCATGT	CATAGGTAAG	TACAACCTCC	TTGGCAAGAA	CTATGCAGGA	2340	
60	TTCAACCCCG	CAACGCGTAA	TGCACAGCAG	TACGAAGCGG	ATGGCAAAGA	ATCGTGGAA	2400

(C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

5

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

10 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
 (B) LOCATION 1...1026

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20

20	AGTTTTATC AAGAAAATAGA CAGACTTATG AAAAAGTATT TGTTATATGC CTCGTTGCTA	60
	ACGAGGTGTT TGCTCTTTTC CTGTTCAAAG AACAAATCCTA ACGAGCCGGT GGAAGACAGA	120
	TCCATCGAAA TTTCTATAAG GGTAGATGAT TTCACCAAAA CGGGTGAGGC AGTACGCTAT	180
	GAAAGGAATC AAGGAAGTGC TGCCGAAAGG CTCATTACCA ATCTTTACCTT CTTGTTGTT	240
	GATCAGTCAG GGGCGAATCC GGGCAAATAC TATATTACCG GTAACACTTT CACCGGAGGG	300
	ACCTGGCTTC CTGACGATAT GAAGGTGAAG TTGGATATGA CACAATCCGA GGCGGGAGAG	360
25	CGCAAAGTAT ATGTCGTAGC CAATGTTGAT AATGCGGTTA AAACGGCTCT TGATGCTGTC	420
	GCTAACGAAA GCGATTGCA GACTGTAAAG AGGACGACTG CAATGCCGTG GTCGACCGAT	480
	ATAGCCTCTC CTTTCCTGAT GTCCGGAAAC AAGACACACG ACTTCTTGGC CAATCGTCTT	540
	TTGGACAATG TGCCCCTTGT GCGTGCCATT GCCAAGGTGG AGCTGAATAT CTCGCTGAGT	600
	GAGAAATTTC AGATTGTGCC GATAATTGTC AATGGTAGTT TGAGTGAGTT CAAGTTCAGA	660
30	TACGTAAACT TCGACAAGGA GACCTACGTA GTGAAGCCAA CGACCAAGCC GGACAATCTC	720
	ATTAGTTCTG CTAATGGTGT TTGGCCTCAG ATTACAGATT GGACTGTATG GGGTGCTTCC	780
	TTAAATACTT CTCCCTGCTCC GGATGCGGGC ACAGGTTATA CATTGGATGC AAATGGCAAG	840
	GTAACGGCAC TACGGATTGT TACCTATCTG AATGAGCGCG ATAGCAAAGG GGCTACGGTA	900
	GAGGTCGCAT TGCCTCGTGT GGATGATGGC ACCCTTCCTC CTCCGGAATT CGGTCCGGAG	960
35	CTTTATCGTT TGCCTTTGCC GGACAAGATC CTGCGCAATC ATTGGTACAA GTATGAAGTC	1020
	GAGATT	1026

(2) INFORMATION FOR SEQ ID NO:21

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2634 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

50

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

55

(ix) FEATURE:

(A) NAME/KEY: misc_feature
 (B) LOCATION 1...2634

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Porphyromonas gingivalis*

5 (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...618

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22

AAACAGATAG TTATGACAGT AAAGCGCGCA GTGCGAATAG CACTTCTCAC GCTGATAGGC	60
ATTCTTTTT CCTCACCTTC TCTTGTTCGG GCGCAAAGTC TTTTCAGCAC CGAACATGTC	120
TTGCAACTAT ACAACAAGAT ACTCTATGGA GAGTCGGCAGG CGGATACCGT CGCAGAGAAA	180
ACGGCAGGTG AGTCGGCATT TCCTTTATA GACAAACTCA TCAATCTCGG CCGCACTTTC	240
15 CTCGGCAAAC CATATCGTA TCGCGGTCTT TCCCCATGGC CGATGGACTG CTCGGGCTAT	300
GTGTCTTACC TCTACTCCAA ATTGACATC AAACCTCCAC GTGGTGCGGC AGCACAGAGC	360
CAATATACGA ATCCTATCGA GCGCGAGGAT GTTCGTCGG GCGACCTCCT TTTTTCAAA	420
GGCCGCAATG CACGCAGCAA CCGTATCGGG CATGTAGCTT TGTCGTATC TGTCGATGAA	480
20 GATGATATTA CCATGATGCA CAGCCGCAAT TCGCGAGGGA TCGTGATCGA AAAACTCAAT	540
CGCAGTGCAT ACTTCTCCCG TCGCTTGGTG AGCTATGGCA GGGTACCCGG AGCCAAGAGA	600
GTGATCCCAC GAAAAAGT	618

25 (2) INFORMATION FOR SEQ ID NO:23

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 342 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

40 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...342

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23

Asn Arg Asn Arg Asn Met Ser Lys Lys Ser Ile Leu Leu Leu Cys Cys	
45 1 5 10 15	
Ser Leu Cys Phe Ile Ser Ala Thr Lys Ala Val Thr Pro Val Arg Asn	
20 20 25 30	
Val Arg Asn Ser Gln Val Asn Ser Lys Ala Lys Thr Glu Arg Thr Lys	
35 35 40 45	
50 Pro Ser Asp Ser Val Arg Tyr Ile Ser Asn Met Ile Ala Asp Arg Leu	
55 55 60	
Glu Phe Arg Asn Lys Ile Ser Ser Glu Lys Glu Val Arg Lys Ala Glu	
65 65 70 75 80	
Tyr Glu Asn Arg Leu Ala Met Glu Ala Leu Asn Tyr Pro Ala Ile Asp	
85 85 90 95	
Leu Tyr Gly Glu Asp Ser Trp Ser Glu Tyr Val Asn Pro Phe Val Gly	
100 100 105 110	
Ala Gly Thr Asp Val Glu Ile Pro Asn Ser Tyr Asp Ile Asp Cys Ser	
115 115 120 125	
60 Ser Phe Val Met Pro Val Glu Asp Lys Gln Val Thr Ser Gln Phe Gly	

Ser Asn Ala Arg Ala Leu Asp Leu Arg Tyr Glu Asp Glu Leu His Arg
 100 105 110
 Val Ile Ile His Gly Ile Leu His Leu Cys Gly Leu Lys Asp Lys Ser
 115 120 125
 5 Lys Lys Asp Glu Ala Gln Met Arg Ala Ala Glu Glu Lys Ala Leu Val
 130 135 140
 Met Leu Arg Glu Thr Ile Gly Ser Glu Leu Ser Leu Leu His Thr
 145 150 155

10 (2) INFORMATION FOR SEQ ID NO:25

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 395 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- 20 (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Porphyromonas gingivalis*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...395
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25

30 Lys Ser Lys Thr Met Lys Val Tyr Leu Met Leu Thr Leu Val Gly
 1 5 10 15
 Ala Ile Ala Leu Asn Ala Ser Ala Gln Glu Asn Thr Val Pro Ala Thr
 20 25 30
 Gly Gln Leu Pro Ala Lys Asn Val Ala Phe Ala Arg Asn Lys Ala Gly
 35 35 40 45
 Ser Asn Trp Phe Val Thr Leu Gln Gly Gly Val Ala Ala Gln Phe Leu
 50 55 60
 Asn Asp Asn Asn Asn Lys Asp Leu Met Asp Arg Leu Gly Ala Ile Gly
 65 70 75 80
 40 Ser Leu Ser Val Gly Lys Tyr His Ser Pro Phe Phe Ala Thr Arg Leu
 85 90 95
 Gln Ile Asn Gly Gly Gln Ala His Thr Phe Leu Gly Lys Asn Gly Glu
 100 105 110
 Gln Glu Ile Asn Thr Asn Phe Gly Ala Ala His Phe Asp Phe Met Phe
 45 115 120 125
 Asp Val Val Asn Tyr Phe Ala Pro Tyr Arg Glu Asn Arg Phe Phe His
 130 135 140
 Leu Ile Pro Trp Val Gly Val Gly Tyr Gln His Lys Phe Ile Gly Ser
 145 150 155 160
 50 Glu Trp Ser Lys Asp Asn Val Glu Ser Leu Thr Ala Asn Val Gly Val
 165 170 175
 Met Met Ala Phe Arg Leu Gly Lys Arg Val Asp Phe Val Ile Glu Ala
 180 185 190
 Gln Ala Ala His Ser Asn Leu Asn Leu Ser Arg Ala Tyr Asn Ala Lys
 195 200 205
 Lys Thr Pro Val Phe Glu Asp Pro Ala Gly Arg Tyr Tyr Asn Gly Phe
 210 215 220
 Gln Gly Met Ala Thr Ala Gly Leu Asn Phe Arg Leu Gly Ala Val Gly
 225 230 235 240
 60 Phe Asn Ala Ile Unk Pro Met Asp Tyr Ala Leu Ile Asn Asp Leu Asn

Asn Ala Asn Gly Glu Lys Val Gly Ser Lys Asp Asp Met Thr Gly Thr
 165 170 175
 Val Asn Val Gly Leu Met Leu Lys Phe Arg Leu Ser Arg Val Val Asp
 180 185 190
 5 Phe Asn Ile Glu Gly Gln Ala Phe Ala Gly Lys Met Asn Phe Ile Gly
 195 200 205
 Thr Lys Arg Gly Lys Ala Asp Phe Pro Val Met Ala Thr Ala Gly Leu
 210 215 220
 Thr Phe Asn Leu Gly Lys Thr Glu Trp Thr Glu Ile Val Pro Met Asp
 10 225 230 235 240
 Tyr Ala Leu Val Asn Asp Leu Asn Asn Gln Ile Asn Ser Leu Arg Gly
 245 250 255
 Gln Val Glu Leu Ser Arg Arg Pro Val Ser Cys Pro Glu Cys Pro
 260 265 270
 15 Glu Pro Thr Gln Pro Thr Val Thr Arg Val Val Asn Val Val
 275 280 285
 Tyr Phe Arg Ile Asn Ser Ala Lys Ile Asp Arg Asn Gln Glu Ile Asn
 290 295 300
 Val Tyr Asn Thr Ala Glu Tyr Ala Lys Thr Asn Asn Ala Pro Ile Lys
 20 305 310 315 320
 Val Val Gly Tyr Ala Asp Glu Lys Thr Gly Thr Ala Ala Tyr Asn Met
 325 330 335
 Lys Leu Ser Glu Arg Arg Ala Lys Ala Val Ala Lys Met Leu Glu Lys
 340 345 350
 25 Tyr Gly Val Ser Ala Asp Arg Ile Thr Ile Glu Trp Lys Gly Ser Ser
 355 360 365
 Glu Gln Ile Tyr Glu Glu Asn Ala Trp Asn Arg Ile Val Val Met Thr
 370 375 380
 Ala Ala Glu
 30 385

(2) INFORMATION FOR SEQ ID NO:27

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 195 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: protein

45 (iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Porphyromonas gingivalis*

50 (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...195

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27

Val Ile Gly Ile Ile Met Glu Phe Phe Met Leu Phe Ile Ala Ala Val
 1 5 10 15
 Phe Val Asn Asn Val Val Leu Ser Gln Phe Leu Gly Ile Cys Pro Phe
 55 20 25 30
 Leu Gly Val Ser Lys Lys Val Asp Thr Ser Ile Gly Met Gly Ala Ala
 35 40 45
 Val Thr Phe Val Leu Ala Leu Ala Thr Leu Val Thr Phe Leu Ile Gln
 50 55 60
 60 Lys Phe Val Leu Asp Arg Phe Gly Leu Gly Phe Met Gln Thr Ile Ala

	Val	Leu	Ser	Pro	Glu	Leu	Phe	Leu	Lys	Thr	Asn	Ser	Thr	Asn	Leu	Ser
				180					185						190	
	Gln	Gly	Leu	Lys	Phe	Gln	Pro	Gly	Leu	Arg	Val	Glu	Asp	Asn	Cys	Gln
				195					200						205	
5	Asn	Cys	Gly	Phe	Asn	Gln	Val	Arg	Ile	Asn	Gly	Leu	Glu	Gly	Ala	Tyr
				210					215						220	
	Ser	Gln	Ile	Leu	Ile	Asp	Ser	His	Pro	Ile	Phe	Ser	Ser	Leu	Ala	Gly
				225					230						235	240
10	Val	Tyr	Gly	Leu	Glu	Gln	Met	Pro	Ala	Asn	Met	Ile	Glu	Arg	Val	Glu
				245					250						255	
	Val	Ile	Arg	Gly	Gly	Ser	Ala	Leu	Phe	Gly	Ser	Asn	Ala	Val	Gly	
				260					265						270	
	Gly	Val	Ile	Asn	Val	Ile	Thr	Lys	Glu	Pro	Leu	Arg	Asn	Ser	Ala	Glu
				275					280						285	
15	Ile	Ser	His	Ser	Thr	Met	Thr	Phe	Asp	His	Ala	Lys	Gly	Trp	Gly	Ser
				290					295						300	
	Phe	Gln	Asn	Thr	Thr	Gln	Phe	Asn	Gly	Ser	Met	Leu	Thr	Glu	Asp	Arg
				305					310						315	320
20	Lys	Ala	Gly	Val	Met	Val	Phe	Gly	Gln	His	Asn	Tyr	Arg	Pro	Gly	Gln
				325					330						335	
	Asp	Ile	Asp	Gly	Asp	Asn	Phe	Thr	Glu	Leu	Pro	Asn	Leu	Arg	Asn	Arg
				340					345						350	
	Ser	Leu	Gly	Phe	Arg	Ser	Tyr	Tyr	Lys	Thr	Gly	Leu	Tyr	Ser	Lys	Ala
				355					360						365	
25	Thr	Leu	Glu	Tyr	His	Ser	Met	Gln	Glu	Tyr	Arg	Arg	Gly	Gly	Asp	Arg
				370					375						380	
	Leu	Asp	Asn	Pro	Pro	Phe	Glu	Ala	Gln	Ile	Ala	Glu	Tyr	Leu	Gln	His
				385					390						395	400
30	Tyr	Ile	Asn	Gly	Gly	Ser	Phe	Lys	Phe	Asp	Gln	Gly	Phe	Ser	Gly	Gly
				405					410						415	
	Lys	Asp	Phe	Phe	Ser	Leu	Tyr	Ala	Ser	Ala	Gln	Asp	Val	Gln	Arg	Arg
				420					425						430	
	Ser	Tyr	Tyr	Gly	Gly	Asp	Tyr	Thr	Glu	Asn	Leu	Leu	Asn	Gly	Ala	
				435					440						445	
35	Val	Gln	Ser	Gly	Ser	Thr	Glu	Ser	Asp	Glu	Tyr	Asn	Asp	Ala	Phe	Thr
				450					455						460	
	Ala	Leu	Thr	Ser	Tyr	Gly	Thr	Thr	Lys	Gly	Phe	Asp	Leu	Gln	Gly	
				465					470						475	480
40	Gly	Met	Tyr	Arg	His	Thr	Phe	Gly	Glu	Asn	Trp	Asp	Phe	Thr	Gly	Gly
				485					490						495	
	Leu	Glu	Tyr	Ile	Tyr	Gly	Gln	Leu	Asp	Asp	Arg	Ser	Gly	Tyr	Arg	Pro
				500					505						510	
	Ser	Lys	Ile	Asp	Gln	Asn	Thr	Ser	Thr	Phe	Ser	Gln	Tyr	Asp	Gln	Leu
				515					520						525	
45	Glu	Tyr	Lys	Thr	Glu	Lys	Leu	Ser	Ala	Leu	Ile	Gly	Ala	Arg	Ile	Asp
				530					535						540	
	Tyr	Val	Leu	Leu	Asn	Gln	Asp	Gly	Lys	Arg	Tyr	Ile	Asp	Pro	Leu	Phe
				545					550						555	560
50	Ile	Phe	Ser	Pro	Arg	Ala	Asn	Val	Arg	Tyr	Asn	Pro	Asn	Lys	Asn	Leu
				565					570						575	
	Ser	Phe	Arg	Leu	Ser	Tyr	Ser	Glu	Gly	Phe	Arg	Ala	Pro	Gln	Tyr	Phe
				580					585						590	
	Asp	Glu	Asp	Leu	His	Val	Glu	Leu	Ala	Gly	Gly	Thr	Pro	Ile	Ser	Arg
				595					600						605	
55	Val	Leu	Ser	Pro	Asn	Leu	Lys	Glu	Glu	Arg	Ser	Arg	Ser	Ile	Ser	Ala
				610					615						620	
	Ser	Phe	Asp	Tyr	Tyr	His	Arg	Ala	Asp	Glu	Trp	Gln	Phe	Asn	Ile	Met
				625					630						635	640
60	Gly	Glu	Ala	Phe	Ser	Thr	Phe	Ile	Ser	Asn	Gln	Phe	Lys	Pro	Ser	Asp
				645					650						655	

	85	90	95
	Ile Met Arg Gln Gly Tyr Phe Ser Asn Val Arg Ile Ile Ala Asp Lys		
	100 105 110		
5	Tyr Val Gly Asn Lys Val Tyr Leu Lys Ile Ile Val Thr Glu Arg Pro		
	115 120 125		
	Arg Ile Ser Lys Val Thr Phe Ser Gly Val Lys Lys Ser Glu Arg Glu		
	130 135 140		
	Asp Leu Glu Met Lys Ile Gly Leu Arg Glu Gly Ile Gln Met Thr Arg		
	145 150 155 160		
10	Asn Asn Glu Asp Lys Val Arg Gln Ile Val Gln Lys Tyr Phe Ser Glu		
	165 170 175		
	Lys Gly Tyr Arg Asp Ala Ser Ile Arg Ile Thr Gln Glu Pro Asp Leu		
	180 185 190		
15	Ser Lys Asp Gly Phe Val Asn Val Leu Ile Ser Ile Glu Lys Lys Ser		
	195 200 205		
	Lys Thr Lys Val Asn Glu Ile Tyr Phe Ser Gly Asn Lys Ala Leu Ser		
	210 215 220		
	Asn His Lys Leu Arg Met Ala Met Lys Asn Thr Asn Ala Lys Phe Ser		
	225 230 235 240		
20	Leu Arg Lys His Ile Arg Ser Ser Phe Leu Lys Leu Phe Ser Thr His		
	245 250 255		
	Lys Phe Val Glu Glu Ser Tyr Arg Glu Asp Leu Val Arg Leu Ile Glu		
	260 265 270		
25	Lys Tyr Gln Glu Tyr Gly Tyr Arg Asp Ala Glu Ile Leu Thr Asp Ser		
	275 280 285		
	Val Val Lys Ala Pro Asp Gly Lys Arg Val Asp Ile Tyr Leu Asn Ile		
	290 295 300		
	Glu Glu Gly Gln Lys Tyr Tyr Ile Lys Asp Val Asn Phe Val Gly Asn		
	305 310 315 320		
30	Ser Gln Tyr Pro Ser Glu Tyr Leu Glu Arg Val Leu Gly Ile Lys Ser		
	325 330 335		
	Gly Asp Val Tyr Asn Gln Arg Arg Leu Ala Lys Arg Leu Asn Glu Asp		
	340 345 350		
35	Glu Asp Ala Val Gly Asn Leu Tyr Tyr Asn Asn Gly Tyr Ile Phe Ala		
	355 360 365		
	Trp Val Asp Pro Val Glu Thr Asn Val Val Gly Asp Ser Val Ser Leu		
	370 375 380		
	Asp Ile Arg Ile Ala Glu Gly Lys Gln Ala Asn Ile Asn Lys Val Ile		
	385 390 395 400		
40	Ile Lys Gly Asn Thr Val Val Tyr Glu Asp Val Val Arg Arg Glu Leu		
	405 410 415		
	Tyr Thr Lys Pro Gly Gln Leu Phe Ser Arg Glu Asp Ile Ile Asn Ser		
	420 425 430		
45	Ile Arg Leu Ile Asn Gln Leu Gly His Phe Asp Ala Glu Lys Ser Ile		
	435 440 445		
	Pro Arg Pro Ile Pro Asn Pro Glu Thr Gly Thr Val Asp Ile Glu Tyr		
	450 455 460		
	Asp Leu Val Pro Arg Ser Ser Asp Gln Leu Glu Leu Ser Val Gly Trp		
	465 470 475 480		
50	Ser Gln Ser Gly Leu Leu Phe Arg Gly Ala Ile Lys Phe Thr Asn Phe		
	485 490 495		
	Ser Val Gly Asn Leu Leu His Pro Ser Met Tyr Lys Lys Gly Ile Ile		
	500 505 510		
55	Pro Gln Gly Asp Gly Gln Thr Leu Ser Leu Ser Ala Gln Thr Asn Gly		
	515 520 525		
	Lys Tyr Tyr Gln Gln Tyr Ser Val Thr Phe Met Asp Pro Trp Phe Gly		
	530 535 540		
	Gly Lys Arg Pro Asp Met Phe Ser Phe Ser Ala Phe Tyr Ser Lys Thr		
	545 550 555 560		
60	Thr Ala Ile Asp Ser Lys Phe Tyr Asn Ser Asn Ala Gly Asn Tyr Tyr		

(B) LOCATION 1...177

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30

5 Gln Ile Asn Met Asn Gly Asp Met Lys Arg Phe Leu Ile Leu Ile Gly
 1 5 10 15
 Phe Ala Leu Ala Val Ala Phe Ser Gly Phe Ser Gln Lys Phe Ala Leu
 20 25 30
 Val Asp Met Glu Tyr Ile Leu Arg Asn Ile Pro Asp Tyr Glu Met Met
 10 35 40 45
 Asn Glu Gln Leu Glu Gln Val Ser Lys Lys Trp Gln Asn Glu Ile Glu
 50 55 60
 Ala Leu Glu Asn Glu Ala Gln Ser Met Tyr Lys Lys Tyr Gln Ser Asp
 65 70 75 80
 15 Leu Val Phe Leu Ser Ala Ala Gln Lys Lys Thr Gln Glu Glu Ala Ile
 85 90 95
 Val Lys Lys Glu Gln Gln Ala Ser Glu Leu Lys Arg Lys Tyr Phe Gly
 100 105 110
 Pro Glu Gly Glu Leu Tyr Lys Lys Arg Ser Asp Leu Met Lys Pro Ile
 20 115 120 125
 Gln Asp Glu Ile Trp Asn Ala Ile Lys Glu Ile Ala Lys Arg Asn Asn
 130 135 140
 Tyr Gln Met Val Leu Asp Arg Gly Thr Ser Gly Ile Ile Phe Ala Ser
 145 150 155 160
 25 Pro Ser Ile Asp Ile Ser Asp Leu Val Leu Ser Lys Met Gly Phe Ser
 165 170 175
 Lys

30 (2) INFORMATION FOR SEQ ID NO:31

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- 35 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

40 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Porphyromonas gingivalis*

45 (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...170

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31

50 Arg Ile Asn Lys Gln His Glu Met Lys Lys Phe Phe Leu Met Leu Leu
 1 5 10 15
 Met Ala Leu Pro Leu Ser Leu Leu Ala Gln Lys Val Ala Val Val Asn
 20 25 30
 Thr Glu Glu Ile Ile Ser Lys Met Pro Glu Gln Val Ala Ala Thr Lys
 55 35 40 45
 Gln Leu Asn Glu Leu Ala Glu Lys Tyr Arg Leu Asp Leu Lys Ser Met
 50 55 60
 Asp Asp Glu Phe Ala Lys Lys Thr Glu Glu Phe Val Lys Glu Lys Asp
 65 70 75 80
 60 Ser Leu Leu Glu Asn Ile Arg Asn Arg Arg Gln Gln Glu Leu Gln Asp

Gly Gly Phe Thr Ala Asp Tyr Gly Asp Lys Met Ser Ser Val Leu Asp
 225 230 235 240
 Ile Arg Tyr Lys Gln Pro Gln Glu Lys Glu Gly Ala Val Leu Leu Gly
 245 250 255
 5 Met Leu Gln Ser Ser Ala Tyr Tyr Gly Ser Ser Ala Gly Ala Phe Ser
 260 265 270
 Gln Ile Thr Gly Val Arg Tyr Lys Ser Ala Lys Ser Leu Leu Gly Thr
 275 280 285
 10 Thr Asp Thr Lys Ala Glu Tyr Asp Pro Ile Tyr Ala Asp Gly Gln Thr
 290 295 300
 Phe Met Thr Tyr Arg Phe Ser Pro Lys Leu Ser Val Ser Phe Leu Gly
 305 310 315 320
 Asn Ile Ser Gln Thr Arg Tyr Lys Phe Val Pro Gln Thr Arg Glu Thr
 325 330 335
 15 Ser Phe Gly Thr Leu Ser Asp Ala Lys Lys Leu Lys Ile Phe Phe Asp
 340 345 350
 Gly Gln Glu Gln Asp Arg Phe Leu Thr Tyr Phe Gly Ala Phe Ser Met
 355 360 365
 20 Asn Phe Val Pro Asp Asp Lys Gln Arg His Thr Val Thr Leu Ser Ala
 370 375 380
 Phe Asn Ser Asn Glu Arg Glu Thr Tyr Asp Ile Gln Gly Glu Tyr Phe
 385 390 395 400
 Leu Asn Asp Val Gln Leu Gly Ala Asp Gly Thr Ala Ser Met Ala Ser
 405 410 415
 25 Gly Ser Glu Asn Ser Asn Gly Leu Gly Ile Gly Arg Asn His Glu His
 420 425 430
 Ala Arg Asn Arg Leu Ser Tyr Arg Val Leu Asn Met Gly Tyr Arg Gly
 435 440 445
 30 Glu Met Lys Leu Asn Glu Lys His Arg Leu Gln Ala Gly Val Ser Ala
 450 455 460
 Gln Met Glu Lys Ile Ala Asp His Ile Ser Glu Trp Glu Arg Arg Asp
 465 470 475 480
 Ser Val Gly Tyr Asn Leu Pro His Ser Glu Thr Val Leu Leu Met Tyr
 485 490 495
 35 Asn Asn Leu Tyr Ala Asp Thr Gln Met Arg Gly Thr Arg Leu Ser Ala
 500 505 510
 Phe Val Gln Asp Arg Phe Asn Phe Ser Met Gly Gly Thr Phe Ser
 515 520 525
 40 Leu Ile Pro Gly Ile Arg Ala Ser Trp Trp Ser Phe Asn Lys Glu Leu
 530 535 540
 Leu Val Ser Pro Arg Ile Ser Val Gly Tyr Ser Pro Glu Ser Asn Pro
 545 550 555 560
 Ala Leu Val Leu Arg Ala Ala Gly Leu Tyr Tyr Gln Ala Pro Phe
 565 570 575
 45 Tyr Lys Glu Leu Arg Gln Thr His Lys Asp Ala Glu Gly Asn Asn Val
 580 585 590
 Val Val Leu Asn Glu Lys Ile Arg Ser Gln Gly Ala Phe His Ile Leu
 595 600 605
 50 Ala Gly Ala Asp Tyr Thr Phe Glu Met Gly Gly Arg Lys Tyr Lys Phe
 610 615 620
 Thr Ala Glu Ala Tyr Tyr Lys Ser Leu Phe Asn Ile Asn Pro Tyr Ile
 625 630 635 640
 Ile Glu Asn Val Lys Ile Arg Tyr Leu Gly Glu Asn Ile Gly Ser Gly
 645 650 655
 55 Tyr Ala Ala Gly Ile Asp Leu Lys Leu Phe Gly Glu Leu Val Pro Gly
 660 665 670
 Val Asp Ser Trp Leu Thr Ala Ser Ile Ile Lys Ala Arg Gln Lys Leu
 675 680 685
 60 Asp Gly Tyr Gly Ser Leu Pro Leu Met Asn Ala Pro Thr Tyr Asn Phe
 690 695 700

	180	185	190
	Gln Ala Asp Val Thr Leu Thr Tyr Phe His Thr Asp His Lys Asp Leu		
	195 200 205		
5	Ile Leu Ser Ser Pro Asp Tyr Ala Asn Asn Ile Thr Thr Tyr Ile Asn		
	210 215 220		
	Ala Asp Lys Ala Arg Met Ser Gly Ile Glu Ala Leu Leu Ser Tyr Asp		
	225 230 235 240		
	Phe Gly Ser Leu Phe Ala Asn Lys Phe Ser Leu Arg Ala Phe Ala Asn		
	245 250 255		
10	Ala Thr Ile Met Leu Asn Ser Glu Met Lys Lys Ser Gln Thr Asp Ala		
	260 265 270		
	Pro Trp Ser Glu Met Tyr Tyr Val Arg Lys Gln Asn Ile Thr Phe Gly		
	275 280 285		
15	Ile Glu Tyr Arg Gly Lys Glu Gly Leu Glu Val Met Leu Asn Gly Arg		
	290 295 300		
	Phe Met Gly Arg Arg Ile Glu Gln Asn Trp Tyr Ala Tyr Tyr Pro Glu		
	305 310 315 320		
	Val Arg Pro Glu Leu Gln Gln Leu Leu Ala Ala Glu Glu Pro Glu Leu		
	325 330 335		
20	Ala Ala Gln Gly Leu Leu Arg His Pro Gln Ala Met Val Phe Asn Ala		
	340 345 350		
	Ser Ala Tyr Tyr His Met Asn Lys Tyr Leu Thr Phe Gly Val Asn Leu		
	355 360 365		
25	Asn Asn Ile Leu Asp Glu Leu Tyr Thr Glu Lys Asp Gly Tyr His Met		
	370 375 380		
	Pro Gly Arg Asn Ile Met Gly Lys Val Met Val Asn Phe		
	385 390 395		

(2) INFORMATION FOR SEQ ID NO:34

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 484 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: protein

 (iii) HYPOTHETICAL: YES

40 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Porphyromonas gingivalis*

45 (ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...484

 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34

	Gly Arg Ala Ser Ser Pro Tyr Arg Gln Met Asp Gly Ile Leu Asn Asp		
50	1 5 10 15		
	Glu Tyr Arg Gln Ala Ser Met Asn Arg Phe Ser Asn His Trp Pro Cys		
	20 25 30		
	Ile Leu Val Gly Phe Val Leu Trp Phe Val Ser Ala Ser Arg Thr Val		
	35 40 45		
55	Ala Gln Asn Ala Ser Glu Thr Thr Val Ser Tyr Asp Thr Asp Thr Ala		
	50 55 60		
	Val Leu Ser Glu Ala Asp Val Leu Arg Ile Ala Leu Ser Glu Asn Ala		
	65 70 75 80		
60	Thr Val Lys Val Ala Asp Met Asp Val Arg Lys Gln Glu Tyr Ala Arg		
	85 90 95		

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

5

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...540

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35

	Phe	His	Asn	Phe	Asp	Phe	Leu	Asn	Gly	Ile	Lys	Leu	Phe	Ser	Met	Ala
1				5					10						15	
15	Asn	Asn	Thr	Leu	Leu	Ala	Lys	Thr	Arg	Arg	Tyr	Val	Cys	Leu	Val	Gly
				20					25						30	
	Phe	Cys	Trp	Leu	Met	Ala	Met	Met	His	Leu	Ser	Gly	Gln	Glu	Val	Thr
				35					40						45	
20	Met	Trp	Gly	Asp	Ser	His	Gly	Val	Ala	Pro	Asn	Gln	Val	Arg	Arg	Thr
				50				55				60				
25	Leu	Val	Lys	Val	Ala	Leu	Ser	Glu	Ser	Leu	Pro	Pro	Gly	Ala	Lys	Gln
				65				70			75				80	
	Ile	Arg	Ile	Gly	Phe	Ser	Leu	Pro	Lys	Glu	Thr	Glu	Glu	Lys	Val	Thr
				85					90						95	
30	Ala	Leu	Tyr	Leu	Leu	Val	Ser	Asp	Ser	Leu	Ala	Val	Arg	Asp	Leu	Pro
				100					105						110	
	Asp	Tyr	Lys	Gly	Arg	Val	Ser	Tyr	Asp	Ser	Phe	Pro	Ile	Ser	Lys	Glu
				115				120							125	
	Asp	Arg	Thr	Thr	Ala	Leu	Ser	Ala	Asp	Ser	Val	Ala	Gly	Arg	Arg	Phe
				130				135							140	
35	Phe	Tyr	Leu	Ala	Ala	Asp	Ile	Gly	Pro	Val	Ala	Ser	Phe	Ser	Arg	Ser
				145				150			155				160	
	Asp	Thr	Leu	Thr	Ala	Arg	Val	Glu	Glu	Val	Ala	Val	Asp	Gly	Arg	Pro
				165					170						175	
40	Leu	Pro	Leu	Lys	Glu	Leu	Ser	Pro	Ala	Ser	Arg	Arg	Leu	Tyr	Arg	Gly
				180					185						190	
	Tyr	Glu	Ala	Leu	Phe	Val	Pro	Gly	Asp	Gly	Gly	Ser	Arg	Asn	Tyr	Arg
				195				200							205	
45	Ile	Pro	Ala	Ile	Leu	Lys	Thr	Ala	Asn	Gly	Thr	Leu	Ile	Ala	Met	Ala
				210				215							220	
50	Asp	Arg	Arg	Lys	Tyr	Asn	Gln	Thr	Asp	Leu	Pro	Glu	Asp	Ile	Asp	Ile
				225				230			235				240	
	Val	Met	Arg	Arg	Ser	Thr	Asp	Gly	Gly	Lys	Ser	Trp	Ser	Asp	Pro	Arg
				245					250						255	
55	Ile	Ile	Val	Gln	Gly	Glu	Gly	Arg	Asn	His	Gly	Phe	Gly	Asp	Val	Ala
				260					265						270	
	Leu	Val	Gln	Thr	Gln	Ala	Gly	Lys	Leu	Leu	Met	Ile	Phe	Val	Gly	Gly
				275					280						285	
60	Val	Gly	Leu	Trp	Gln	Ser	Thr	Pro	Asp	Arg	Pro	Gln	Arg	Thr	Tyr	Ile
				290				295							300	
	Ser	Glu	Ser	Arg	Asp	Glu	Gly	Leu	Thr	Trp	Ser	Pro	Pro	Arg	Asp	Ile
				305				310			315				320	
	Thr	His	Phe	Ile	Phe	Gly	Lys	Asp	Cys	Ala	Asp	Pro	Gly	Arg	Ser	Arg
				325					330						335	
55	Trp	Leu	Ala	Ser	Phe	Cys	Ala	Ser	Gly	Gln	Gly	Leu	Val	Leu	Pro	Ser
				340					345						350	
	Gly	Arg	Ile	Thr	Phe	Val	Ala	Ala	Ile	Arg	Glu	Ser	Gly	Gln	Glu	Tyr
				355					360						365	
60	Val	Leu	Asn	Asn	Tyr	Val	Leu	Tyr	Ser	Asp	Asp	Glu	Gly	Asp	Thr	Trp
				370				375							380	
	Gln	Leu	Ser	Asp	Cys	Ala	Tyr	Arg	Arg	Gly	Asp	Glu	Ala	Lys	Leu	Ser

Glu Gln Asn Val Arg Thr Phe Ala Gly Tyr Leu Leu Ser Gln Thr Val
 165 170 175
 Thr Val Thr Ser Gln Asp Ile Glu His Val Glu Lys Ile Ser Arg Asp
 180 185 190
 5 Ile Thr Glu Leu Ile Asn Gln Gly Val Glu Ile Thr Ser Asp Arg Pro
 195 200 205
 Ala Tyr Tyr Tyr Thr Lys Leu Asn Asp Leu Lys Val Glu Met Leu Arg
 210 215 220
 Asn Ala Ser Glu Asp Ala Phe Asn Arg Ala Ser Val Ile Ala Glu Gly
 10 225 230 235 240
 Ser Gly Ser Ser Val Gly Lys Met Leu Ser Ser Met Gly Val Phe
 245 250 255
 Gln Ile Val Gly Leu Asn Ser Asn Glu Asp Tyr Ser Trp Gly Gly Ser
 260 265 270
 15 Phe Asn Thr Ser Ser Lys Met Lys Thr Ala Ser Ile Thr Val Lys Ala
 275 280 285
 Ser Phe Ala Leu Lys
 290

20 (2) INFORMATION FOR SEQ ID NO:37

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 280 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- 30 (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Porphyromonas gingivalis*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...280
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37

40 Gly Lys Leu Gln Met Lys Lys Thr Ile Ala Ile Ile Ala Ser Ala Leu
 1 5 10 15
 Leu Ala Leu Gly Ala Val Gly Cys Lys Lys Asn Ala Asp Thr Thr Ala
 20 25 30
 45 Val Ser Glu Lys Asp Ser Ile Ala Leu Ser Met Gly Ile Leu Tyr Gly
 35 40 45
 Gln Asp Phe Ala Asn Gln Phe Glu Met Ser Arg Leu Gln Gly Gln Pro
 50 55 60
 Ile Asp Ser Val Ala Phe Leu Asp Gly Phe Lys Tyr Gly Ile Asp Thr
 65 70 75 80
 50 Thr Arg Phe Ser Tyr Asn Leu Gly Ala Ile Tyr Ala Ser Asn Ile Ala
 85 90 95
 Arg Gln Leu Ala His Asp Ser Ile Asp Ile Asp Lys Phe Tyr Ala Ala
 100 105 110
 55 Met Arg Ala Ala Leu Leu Lys Asp Thr Val Ser Ile Ala Met Lys Pro
 115 120 125
 Ala Asp Ala Gln Ala Phe Met Gln Arg Ile Gln Ala Lys Lys Gln Arg
 130 135 140
 Glu Asn Asn Met Lys Gln Phe Gly Gln Asn Ile Glu Lys Gly Asn Glu
 145 150 155 160
 60 Tyr Ile Asp Thr Phe Lys Lys Glu Asp Gly Val Thr Val Thr Thr

	His	Tyr	Asp	Ser	Ile	Ile	Pro	Leu	Pro	Ile	Ser	Thr	Phe	Pro	Asp	Ser
	195						200					205				
	Ile	Leu	Ala	Tyr	Arg	Gln	Thr	Pro	Ser	Leu	Ile	Arg	Lys	Gly	Asp	Gln
5	210						215					220				
	Phe	Asn	Leu	Ala	Lys	Leu	His	Glu	Glu	Arg	Gln	Thr	Ile	Ser	Ala	Leu
	225						230					235				240
	Leu	Arg	Asp	Asn	Gly	Tyr	Tyr	Phe	Arg	Pro	Gln	Asp	Ile	Ile	Tyr	
10	245						250					255				
	Glu	Ala	Asp	Thr	Leu	Leu	Val	Gly	Ala	Val	Cys	Leu	Arg	Ala	Lys	
	260						265					270				
	Leu	Ser	Glu	Asp	Thr	Pro	Pro	Gln	Ala	Met	Arg	Pro	Trp	Arg	Ile	Gly
	275						280					285				
	Lys	Arg	Thr	Ala	Val	Leu	Leu	Gly	Met	Asn	Gly	Glu	Ser	Pro	Thr	Asp
15	290						295					300				
	Ser	Leu	Glu	Val	Glu	Asp	Met	Lys	Val	Leu	Tyr	Tyr	Arg	Lys	Met	Pro
	305						310					315				320
	Val	Arg	Pro	Lys	Ile	Leu	Ala	Lys	Arg	Phe	Arg	Phe	Phe	Ser	Gly	Asn
	325						330					335				
20	Leu	Tyr	Arg	Gln	Lys	Asp	Asp	Glu	Thr	Thr	Arg	Lys	Ser	Leu	Ala	Arg
	340						345					350				
	Leu	Gly	Ala	Phe	Ser	Val	Ile	Asp	Leu	Asn	Phe	Leu	Gln	Arg	Asp	Ser
	355						360					365				
	Ile	Ser	Gly	Leu	Leu	Asp	Val	Arg	Leu	Leu	Thr	Thr	Leu	Asp	Lys	Pro
	370						375					380				
25	Trp	Asp	Ala	Ser	Leu	Glu	Thr	Leu	Phe	Thr	Ser	Lys	Ser	Asn	Asp	Phe
	385						390					395				400
	Ile	Gly	Pro	Gly	Leu	Asn	Phe	Ala	Leu	Ala	Arg	Arg	Asn	Val	Phe	Gly
	405						410					415				
30	Gly	Gly	Glu	Asn	Leu	Ser	Trp	Asn	Ile	Gly	Gly	Ser	Tyr	Glu	Trp	Glu
	420						425					430				
	Thr	Gly	Asn	Arg	Pro	Glu	Asn	Ser	Ser	Asn	Arg	Leu	Ile	Asp	Ile	Asn
	435						440					445				
	Ser	Tyr	Asn	Met	Asn	Thr	Ala	Val	Asn	Leu	Ser	Phe	Pro	Ser	Ile	Val
35	450						455					460				
	Phe	Pro	Gly	Leu	Leu	Asp	Lys	Tyr	Tyr	Tyr	Tyr	Pro	Thr	Thr	Thr	Thr
	465						470					475				480
	Phe	Gln	Ala	Ser	Ala	Thr	Ala	Leu	Asn	Arg	Ala	His	Tyr	Phe	Ser	Met
	485						490					495				
40	Tyr	Ser	Phe	Gly	Phe	Ser	Thr	Thr	Tyr	Glu	Phe	Gln	Pro	Ser	Lys	Glu
	500						505					510				
	His	Arg	His	Ala	Ile	Phe	Pro	Leu	Lys	Leu	Asn	Tyr	Asn	Leu	Leu	Gly
	515						520					525				
	His	Gln	Thr	Glu	Thr	Phe	Gln	Ala	Ile	Thr	Ala	Asn	Asn	Pro	Pro	Leu
45	530						535					540				
	Leu	Leu	Ser	Leu	Gln	Ser	Gln	Phe	Leu	Ala	Gln	Met	Gly	Tyr	Ile	Tyr
	545						550					555				560
	Thr	Phe	Asn	Lys	Ser	Val	Ser	Glu	Lys	Ser	Pro	His	His	Leu	Trp	Met
	565						570					575				
50	Gln	Phe	Gly	Leu	Ser	Glu	Ala	Gly	Asn	Leu	Leu	Asn	Leu	Ile	Tyr	Leu
	580						585					590				
	Ala	Ala	Gly	Lys	Lys	Tyr	Ser	Asp	Thr	Lys	Asn	Phe	Val	Gly	Val	Pro
	595						600					605				
	Phe	Ser	Gln	Phe	Ile	Lys	Ala	Thr	Gly	Glu	Leu	Arg	Tyr	Ser	Tyr	Thr
55	610						615					620				
	Ile	Asp	Arg	Asn	Gln	Ser	Leu	Ala	Thr	Arg	Phe	Gly	Thr	Gly	Val	Ile
	625						630					635				640
	Tyr	Ser	Tyr	Gly	Asn	Met	Arg	Val	Ala	Pro	Tyr	Ser	Glu	Gln	Phe	Tyr
	645						650					655				
60	Val	Gly	Gly	Ala	Asn	Ser	Ile	Arg	Ala	Phe	Thr	Val	Arg	Ser	Ile	Gly
	660						665					670				

	165	170	175
	Pro Pro Val Ala Leu Gly Asn Ser	Leu Pro Ser Ala Tyr	Lys Val Gly
	180	185	190
	Ile Ser Glu Gly Ser Pro Leu Ser	Pro Ile Val Leu Asp	Glu Glu Arg
5	195	200	205
	Lys Ala Ile Ala Arg His Met Arg Asn Asn	Gly Phe Trp Lys Phe Ser	
	210	215	220
	Ala Glu Asp Val Tyr Tyr	Glu Ala Asp Thr Thr	Val Ser Gly Gly Ser
	225	230	235
10	Gly Thr Lys Ser Ala Asp Leu Lys	Leu Val Val Asn Gly	Ile Gly Arg
	245	250	255
	Tyr Pro Tyr Arg Ile Gly Arg Val	Phe Phe His Ala Asp	Tyr Asp Pro
	260	265	270
15	Leu Glu Ser Asp Phe Arg Val	Gln Glu Leu Pro Arg	Ile Asp Ser Ile
	275	280	285
	Ser Arg Gly Asp Tyr Thr Val	Tyr Gly Ser Arg	Gly Arg Tyr Ile
	290	295	300
	Arg Ala Ser Ala Leu Thr Arg Ser	Val Ser Val Thr	Pro Gly Ala Phe
	305	310	315
20	Phe Cys Glu Asp Asp Val Glu Arg Ser	Tyr Ile Lys	Leu Asn Ala Leu
	325	330	335
	Pro Ile Val Arg Asn Val Asn Ile Arg	Phe Val Glu His Asn	Gly Lys
	340	345	350
25	Asp Glu Ile Ala Leu Ala Asp Ser	Ser Arg Leu Val Asp	Cys Tyr Ile
	355	360	365
	Leu Thr Val Pro Ala Lys Ser	Lys Ser Phe Glu Ala	Glu Val Leu Gly
	370	375	380
	Thr Asn Ser Ala Gly Asp Phe	Gly Ala Ala Leu Ser	Leu Gly Phe Thr
	385	390	395
30	Asp Arg Asn Leu Phe Arg Gly Ala	Glu Met Phe Asn Ile Lys	Leu Lys
	405	410	415
	Gly Ala Tyr Glu Ala Ile Arg Lys	Gly Ser His Ser Phe	Met Glu Tyr
	420	425	430
35	Gly Val Glu Ser Ser Leu Arg	Phe Pro Arg Leu Leu	Phe Pro Phe Ile
	435	440	445
	Ser Asp Glu Thr Arg Arg	Leu Arg Ala Ser Thr	Glu Trp Lys Ile
	450	455	460
	Gly Tyr Asn Tyr Gln Thr Arg Pro	Glu Phe Asp Arg Val	Ile Leu Ser
	465	470	475
40	Ala Gln Leu Asn Tyr Ser Trp Gln	Thr Tyr Leu His Asn Arg	Leu Arg
	485	490	495
	His Thr Ile Arg Leu Leu Asp Val	Asp Tyr Leu His	Leu Pro Tyr Ile
	500	505	510
45	Asp Pro Asp Phe Ala Gln Ser	Leu Pro Pro Thr Thr	Ala Leu Tyr Asn
	515	520	525
	Tyr Thr Glu Gln Phe Ile Leu	Gly Ser Ala Tyr	Ile Leu Asn Tyr Thr
	530	535	540
	Thr Ala Ser Ser Met Glu Arg	Thr Val Ser Asn	Pro Phe Thr Ala Arg
	545	550	555
50	Phe Ser Ile Gln Thr Ala Gly Asn	Leu Leu Gln Ala Ile Ser	Tyr Leu
	565	570	575
	Thr Asp Ser Pro Lys Asp Glu His	Gly Leu Tyr Lys Met	Phe Gly Leu
	580	585	590
55	His Tyr Ala Gln Phe Val Lys	Leu Asp Leu Asp	Leu Ala Lys Thr Val
	595	600	605
	Leu Leu Glu Lys Asp Asn Thr	Leu Ala Leu His	Leu Gly Phe Gly Leu
	610	615	620
	Ala Phe Pro Tyr Gly Asn Ala Arg	His Ile Pro Phe Glu	Leu Arg Tyr
	625	630	635
60	Phe Ala Gly Gly Ser Asn Ser Val	Arg Gly Trp Ser Val	Arg Thr Leu
			640

Arg Thr Asn Val Arg Gly Phe Asp Thr Tyr Asn Phe Gly Val Leu Ile
 180 185 190
 Asn Gly Val Pro Val Asn Gly Met Glu Asp Gly Lys Val Tyr Trp Ser
 195 200 205
 5 Asn Trp Ser Gly Leu Met Asn Gln Ala Ser Thr Ile Gln Ile Gln Arg
 210 215 220
 Gly Leu Gly Ala Ser Lys Leu Gly Ile Ser Ser Val Gly Gly Thr Met
 225 230 235 240
 Asn Ile Ile Thr Lys Thr Asp Ala Asn Thr Gly Gly Ser Ala Tyr
 10 245 250 255
 Val Gly Met Gly Asn Asp Gly Leu His Lys Glu Ser Phe Ser Ile Ser
 260 265 270
 Thr Gly Met Asn Asp Gly Trp Ala Ile Thr Ile Ala Gly Ser His Met
 275 280 285
 15 Thr Gly Leu Gly Tyr Val Lys Gly Leu Lys Gly Arg Ala Phe Ser Tyr
 290 295 300
 Phe Phe Asn Val Ser Lys Lys Phe Asn Glu Arg His Thr Leu Ser Leu
 305 310 315 320
 20 Thr Gly Phe Gly Ala Pro Gln Trp His Asn Gln Arg Ser Ser Lys Tyr
 325 330 335
 Ser Val Ala Asp Tyr Asp Lys Tyr Gly Ile Arg His Asn Gln Ser Phe
 340 345 350
 Gly Tyr Leu Arg Gly Glu Leu Thr Pro Thr Ala Tyr Ala Tyr Asn Thr
 355 360 365
 25 Tyr His Lys Pro Gln Phe Ser Leu Asn His Phe Trp Lys Met Asp Glu
 370 375 380
 Asn Thr Ser Leu Tyr Thr Ala Unk Tyr Ala Ser Leu Ala Thr Gly Gly
 385 390 395 400
 Gly Arg Arg Ala Tyr Gly Lys Asn Ser Lys Trp Val Leu Ile Asn Tyr
 405 410 415
 30 Asn Thr Gly Gln Pro Tyr Glu Gln Thr Lys Val Thr Pro Asp Gly Leu
 420 425 430
 Ile Asp Tyr Asp Ala Val Leu Ala Asn Ala Ala Ser Asn Gly
 435 440 445
 35 Ser Glu Ala Ile Phe Ala Leu Gly Ser Asn Ser His Lys Trp Phe Gly
 450 455 460
 Leu Leu Ser Ser Phe Lys Lys Leu Asn Ser Ser Leu Thr Leu Thr
 465 470 475 480
 40 Ala Gly Tyr Asp Gly Arg Tyr Tyr Arg Gly Asp His Tyr Asp Lys Ile
 485 490 495
 Thr Asp Leu Leu Gly Gly Ser Tyr Tyr Ile Glu Asp Pro Lys Thr Lys
 500 505 510
 Leu Ala Tyr His Ala Glu Gly Gln Gln Leu Lys Val Gly Asp Ile Val
 515 520 525
 45 Asn Arg Asp Tyr Thr Gly Glu Ile Met Trp His Gly Leu Phe Ala Gln
 530 535 540
 Met Glu His Ser Ser Glu Trp Ile Asp Ala Phe Val Ser Gly Ser Ile
 545 550 555 560
 50 Asn Tyr Glu Leu Tyr Arg Asn His Asn Tyr Gly Gly Ser Lys Ser Thr
 565 570 575
 Gly Tyr Leu Pro Gly Val Ser Pro Trp Lys Ser Phe Leu Pro Trp Ser
 580 585 590
 Gly Lys Ala Gly Leu Ser Tyr Lys Phe Ala Gln Gly His Asn Val Phe
 595 600 605
 55 Ala Asn Gly Gly Phe Phe Thr Arg Ala Pro Leu Phe Gly Asn Ile Tyr
 610 615 620
 Ala Ala Gly Ala Ile Ile Pro Asn Asp Lys Ala Asn Met Glu Lys Val
 625 630 635 640
 60 Leu Thr Gly Glu Val Gly Tyr Gly Phe Thr Asn His Lys Asn Phe Glu
 645 650 655

		85		90		95
	Leu Asn Lys Gln Val Ala Gln Arg Lys Gln Met Val Gln Leu Leu Asp					
	100	105			110	
5	Asn Glu Val Lys Glu Leu Gln Ser Asp Ile Asp Ser Met Thr Gly Val	115	120		125	
	Cys His Gln Leu Ser Val Glu Glu Lys Ala Arg Ser Asp Glu Tyr Ala	130	135	140		
	Gln Ala Leu Gln Ser Met Gln Lys Arg Lys Arg Ser Leu Asp Arg Ile	145	150	155		160
10	Leu Phe Ile Ser Ser Ala Lys Ser Phe Asp Glu Gly Met Arg Arg Met	165	170		175	
	Arg Phe Leu Glu Gln Tyr Ala Ser Ala Tyr Lys Leu Ala Ser Val Arg	180	185		190	
15	Leu Arg Asp Thr Arg Ser Lys Leu Glu Thr Glu Arg Ala Thr Val Glu	195	200	205		
	Asp Ala Lys Lys Glu Lys Gly His Leu Leu Val Ile Arg Glu Glu Glu	210	215	220		
	Lys Lys Lys Leu Glu Gly Gln Gln Ala Glu Gln Arg Arg Gln Val Gln	225	230	235		240
20	Ala Leu Gly Ala Lys Gln Lys Asp Leu Glu Ala Gln Leu Arg Lys Gln	245	250		255	
	Lys Lys Gln Ala Glu Ala Leu Asn Arg Lys Ile Glu Lys Gln Ile Ala	260	265		270	
25	Lys Glu Ile Glu Ala Ala Glu Arg Arg Ala Arg Glu Glu Arg Glu Arg	275	280		285	
	Leu Ala Arg Glu Ala Lys Ala Lys Gly Lys Pro Val Pro Ala Glu Pro	290	295	300		
	Glu Arg Lys Ala Glu Thr Lys Gly Gly Tyr Ala Met Asp Ala Ser Glu	305	310	315		320
30	Arg Ala Leu Ser Gly Ser Phe Ala Gln Asn Lys Gly Arg Leu Pro Gly	325	330		335	
	Pro Val Arg Gly Arg Tyr Arg Ile Val Ser Asp Phe Gly Val His Gln	340	345		350	
35	His Ser Glu Leu Lys Lys Val Gln Val Asn Asn Gly Gly Ile Asp Ile	355	360		365	
	Ala Val Ala Thr Gly Ser Asp Ala Thr Ser Val Phe Asp Gly Val Val	370	375	380		
	Ser Ser Val Phe Val Ile Pro Gly Tyr Asn Ser Ala Val Met Val Arg	385	390	395		400
40	His Gly Asn Tyr Ile Thr Val Tyr Ala Asn Leu Ser Lys Val Tyr Val	405	410		415	
	Asn Ser Gly Thr Arg Val Lys Thr Gly Gln Ala Leu Gly Arg Ala Tyr	420	425		430	
45	Thr Asp Pro Ser Asn Asn Gln Thr Ile Ile His Phe Glu Ile Trp Lys	435	440		445	
	Glu Arg Ser Lys Gln Asn Pro Arg Leu Trp Leu Arg	450	455		460	

(2) INFORMATION FOR SEQ ID NO:42

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 342 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

55 (ii) MOLECULE TYPE: protein

 (iii) HYPOTHETICAL: YES

60 (vi) ORIGINAL SOURCE:

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

10 (B) LOCATION 1...878

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43

15	Ala Asp Ser Ile Arg Tyr Pro Leu Tyr Phe Phe Gly Arg Asn Arg Lys 1 5 10 15
	Lys Cys Phe Arg Glu Pro Ile Pro Thr Leu Tyr Asn Lys Asn Met Ile 20 25 30
	Gly Lys Lys Ile Phe Phe Ile Leu Leu Ala Leu Ile Ala Phe Ser Gly 35 40 45
20	Leu Asn Ala Ala Thr Asp Thr Glu Phe Lys Tyr Pro Thr Asp Ala Asn 50 55 60
	Ile Ile Gly His Val Lys Asp Ser Lys Thr Gly Glu His Leu Val Gly 65 70 75 80
25	Ile Thr Ile Ala Ile Lys Gly Thr Thr Phe Gly Thr Ser Thr Asp Ala 85 90 95
	Thr Gly His Tyr Tyr Leu Arg Asn Leu Arg Pro Gly Glu Ile Thr Leu 100 105 110
	Ile Met Arg Gly Met Gly Tyr Lys Ser Gln Glu Arg Val Val Arg Val 115 120 125
30	Glu Lys Asp Lys Thr Ile Glu Val Asn Phe Glu Ala Glu Glu Asp Ala 130 135 140
	Ile Asn Leu Asp Glu Val Val Ile Ser Ala Asn Arg Glu Leu Thr Leu 145 150 155 160
	Arg Arg Leu Ala Pro Thr Leu Val Asn Val Leu Asn Glu Lys Val Phe 165 170 175
35	Ser Gln Val Asn Ala Ser Asn Leu Ala Gln Gly Leu Ser Phe Gln Pro 180 185 190
	Gly Val Arg Val Glu Asn Asn Cys Gln Asn Cys Gly Phe Asn Gln Val 195 200 205
40	Arg Ile Asn Gly Leu Asp Gly Arg Tyr Ala Gln Ile Leu Ile Asp Ser 210 215 220
	Arg Pro Ile Met Ser Ala Leu Ala Gly Val Tyr Gly Leu Glu Gln Ile 225 230 235 240
45	Pro Ala Asn Met Ile Glu Arg Val Glu Val Val Arg Gly Gly Ser 245 250 255
	Ala Leu Tyr Gly Ser Ser Ala Ile Ala Gly Val Val Asn Ile Ile Thr 260 265 270
	Lys Glu Pro Ser His Asn Ser Phe Thr Phe Asn Glu Ser Leu Ser Phe 275 280 285
50	Thr Gly Phe Ser Lys Leu Asp Asn Asn Thr Asn Phe Asn Ala Ser Ile 290 295 300
	Val Ser Asp Asp Asn Arg Ala Gly Ala Met Val Phe Gly Gln Ala Arg 305 310 315 320
55	Tyr Arg Asn His Trp Asp Ala Asn Asn Asp Gly Tyr Ser Glu Leu Gly 325 330 335
	Lys Ile Asp Ala Arg Ser Leu Gly Ala His Ser Tyr Leu Arg Leu Ser 340 345 350
	Asp Tyr Ser Lys Leu Thr Gly Glu Phe His Thr Ile Ser Glu Phe Arg 355 360 365
60	Arg Gly Gly Asp Arg Ile Asp Leu Pro Pro His Val Val Gly Val Ala

850	855	860
Thr Gln Pro Arg Thr Gly Tyr Met Gly Leu Val Val Lys Phe		
865	870	875

5 (2) INFORMATION FOR SEQ ID NO:44

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 206 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

- (iii) HYPOTHETICAL: YES

- 15 (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Porphyromonas gingivalis*

- 20 (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...206

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44

25	Lys Gln Ile Val Met Thr Val Lys Arg Ala Val Arg Ile Ala Leu Leu			
	1	5	10	15
	Thr Leu Ile Gly Ile Leu Phe Ser Ser Pro Ser Leu Val Arg Ala Gln			
	20	25		30
30	Ser Leu Phe Ser Thr Glu His Val Leu Gln Leu Tyr Asn Lys Ile Leu			
	35	40		45
	Tyr Gly Glu Ser Ala Ala Asp Thr Val Ala Glu Lys Thr Ala Gly Glu			
	50	55	60	
35	Ser Ala Phe Pro Phe Ile Asp Lys Leu Ile Asn Leu Gly Arg Thr Phe			
	65	70	75	80
	Leu Gly Lys Pro Tyr Arg Tyr Arg Gly Pro Ser Pro Trp Pro Met Asp			
	85	90		95
	Cys Ser Gly Tyr Val Ser Tyr Leu Tyr Ser Lys Phe Asp Ile Lys Leu			
	100	105		110
40	Pro Arg Gly Ala Ala Ala Gln Ser Gln Tyr Thr Asn Pro Ile Glu Arg			
	115	120	125	
	Glu Asp Val Arg Pro Gly Asp Leu Leu Phe Phe Lys Gly Arg Asn Ala			
	130	135	140	
45	Arg Ser Asn Arg Ile Gly His Val Ala Leu Val Val Ser Val Asp Glu			
	145	150	155	160
	Asp Asp Ile Thr Met Met His Ser Arg Asn Ser Arg Gly Ile Val Ile			
	165	170		175
	Glu Lys Leu Asn Arg Ser Ala Tyr Phe Ser Arg Arg Leu Val Ser Tyr			
	180	185		190
50	Gly Arg Val Pro Gly Ala Lys Arg Val Ile Pro Arg Lys Ser			
	195	200		205

(2) INFORMATION FOR SEQ ID NO:45

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 337 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

(B) TYPE: amino acid
 (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

10 (ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...151

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:46

Met	Ala	Lys	Ile	Asn	Phe	Tyr	Ala	Glu	Gly	Val	Ser	Leu	Pro	Arg	Ile	
1															15	
Arg	Arg	Arg	Ile	Val	Gly	Lys	Trp	Ile	Ala	Glu	Val	Cys	Ser	Arg	Tyr	
															30	
Gly	Lys	Ala	Val	Gly	Glu	Ile	Ser	Tyr	Leu	Phe	Cys	Asp	Asp	Glu	Tyr	
															45	
Ile	Leu	Lys	Ala	Asn	Gln	Glu	Phe	Leu	Asp	His	Asp	Tyr	Tyr	Thr	Asp	
															60	
25	Ile	Ile	Thr	Phe	Asp	Ser	Cys	Glu	Ala	Asp	Thr	Val	Asn	Gly	Asp	Leu
															80	
20	Leu	Ile	Ser	Leu	Asp	Thr	Val	Arg	Ser	Asn	Ala	Arg	Ala	Leu	Asp	Leu
															95	
30	Arg	Tyr	Glu	Asp	Glu	Leu	His	Arg	Val	Ile	Ile	His	Gly	Ile	Leu	His
															110	
35	Leu	Cys	Gly	Leu	Lys	Asp	Lys	Ser	Lys	Lys	Asp	Glu	Ala	Gln	Met	Arg
															125	
40	Ala	Ala	Glu	Lys	Ala	Leu	Val	Met	Leu	Arg	Glu	Thr	Ile	Gly	Ser	
															140	
45	Glu	Leu	Ser	Leu	Leu	His	Thr									

(2) INFORMATION FOR SEQ ID NO:47

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 391 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

45 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

50 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Porphyromonas gingivalis*

55 (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...391

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47

Met	Lys	Val	Lys	Tyr	Leu	Met	Leu	Thr	Leu	Val	Gly	Ala	Ile	Ala	Leu
1															15

60	Asn	Ala	Ser	Ala	Gln	Glu	Asn	Thr	Val	Pro	Ala	Thr	Gly	Gln	Leu	Pro
----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

(A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

5 (B) LOCATION 1...385

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48

10	Met Thr Tyr Arg Ile Met Lys Ala Lys Ser Leu Leu Leu Ala Leu Ala 1 5 10 15
	Gly Leu Ala Cys Thr Phe Ser Ala Thr Ala Gln Glu Ala Thr Thr Gln 20 25 30
	Asn Lys Ala Gly Met His Thr Ala Phe Gln Arg Asp Lys Ala Ser Asp 35 40 45
15	His Trp Phe Ile Asp Ile Ala Gly Gly Ala Gly Met Ala Leu Ser Gly 50 55 60
	Trp Asn Asn Asp Val Asp Phe Val Asp Arg Leu Ser Ile Val Pro Thr 65 70 80
	Phe Gly Ile Gly Lys Trp His Glu Pro Tyr Phe Gly Thr Arg Leu Gln 20 85 95
	Phe Thr Gly Phe Asp Ile Tyr Gly Phe Pro Gln Gly Ser Lys Glu Arg 100 105 110
	Asn His Asn Tyr Phe Gly Asn Ala His Leu Asp Phe Met Phe Asp Leu 115 120 125
25	Thr Asn Tyr Phe Gly Val Tyr Arg Pro Asn Arg Val Phe His Ile Ile 130 135 140
	Pro Trp Ala Gly Ile Gly Phe Gly Tyr Lys Phe His Ser Glu Asn Ala 145 150 160
	Asn Gly Glu Lys Val Gly Ser Lys Asp Asp Met Thr Gly Thr Val Asn 30 165 175
	Val Gly Leu Met Leu Lys Phe Arg Leu Ser Arg Val Val Asp Phe Asn 180 185 190
	Ile Glu Gly Gln Ala Phe Ala Gly Lys Met Asn Phe Ile Gly Thr Lys 195 200 205
35	Arg Gly Lys Ala Asp Phe Pro Val Met Ala Thr Ala Gly Leu Thr Phe 210 215 220
	Asn Leu Gly Lys Thr Glu Trp Thr Glu Ile Val Pro Met Asp Tyr Ala 225 230 240
	Leu Val Asn Asp Leu Asn Asn Gln Ile Asn Ser Leu Arg Gly Gln Val 40 245 255
	Glu Glu Leu Ser Arg Arg Pro Val Ser Cys Pro Glu Cys Pro Glu Pro 260 265 270
	Thr Gln Pro Thr Val Thr Arg Val Val Val Asp Asn Val Val Tyr Phe 275 280 285
45	Arg Ile Asn Ser Ala Lys Ile Asp Arg Asn Gln Glu Ile Asn Val Tyr 290 295 300
	Asn Thr Ala Glu Tyr Ala Lys Thr Asn Asn Ala Pro Ile Lys Val Val 305 310 315 320
	Gly Tyr Ala Asp Glu Lys Thr Gly Thr Ala Ala Tyr Asn Met Lys Leu 50 325 330 335
	Ser Glu Arg Arg Ala Lys Ala Val Ala Lys Met Leu Glu Lys Tyr Gly 340 345 350
	Val Ser Ala Asp Arg Ile Thr Ile Glu Trp Lys Gly Ser Ser Glu Gln 355 360 365
55	Ile Tyr Glu Glu Asn Ala Trp Asn Arg Ile Val Val Met Thr Ala Ala 370 375 380
	Glu 385

60 (2) INFORMATION FOR SEQ ID NO:49

(B) LOCATION 1...833

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50

5 Met Lys Gln Leu Asn Ile Ile Ser Phe Ile Ile Ala Phe Leu Phe Leu
 1 5 10 15
 Gly Thr Ser Ala Ser Ala Gln Gln Ser Gly Gly Ser Val Thr Gly Thr
 20 25 30
 Val Val Asp Lys Ser Ser Lys Glu Pro Ile Ala Tyr Val Gln Val Phe
 10 35 40 45
 Val Lys Gly Thr Thr Leu Gly Thr Ser Thr Asp Ala Asn Gly Asn Tyr
 50 55 60
 Ser Ile Lys Gly Ile Pro Ser Gly Asn Gln Thr Ile Val Ala Arg Leu
 65 70 75 80
 15 Met Gly Tyr Ser Thr Cys Glu Glu Lys Val His Ile Glu Lys Gly Gly
 85 90 95
 Ser Arg His Val Asp Leu Tyr Leu Thr Glu Glu Ile Leu Ser Leu Asp
 100 105 110
 Gly Val Val Val Ser Ala Asn Arg Asn Glu Thr Phe Arg Arg Gln Ala
 20 115 120 125
 Pro Ser Leu Val Thr Val Leu Ser Pro Glu Leu Phe Leu Lys Thr Asn
 130 135 140
 Ser Thr Asn Leu Ser Gln Gly Leu Lys Phe Gln Pro Gly Leu Arg Val
 145 150 155 160
 25 Glu Asp Asn Cys Gln Asn Cys Gly Phe Asn Gln Val Arg Ile Asn Gly
 165 170 175
 Leu Glu Gly Ala Tyr Ser Gln Ile Leu Ile Asp Ser His Pro Ile Phe
 180 185 190
 Ser Ser Leu Ala Gly Val Tyr Gly Leu Glu Gln Met Pro Ala Asn Met
 30 195 200 205
 Ile Glu Arg Val Glu Val Ile Arg Gly Gly Ser Ala Leu Phe Gly
 210 215 220
 Ser Asn Ala Val Gly Gly Val Ile Asn Val Ile Thr Lys Glu Pro Leu
 225 230 235 240
 35 Arg Asn Ser Ala Glu Ile Ser His Ser Thr Met Thr Phe Asp His Ala
 245 250 255
 Lys Gly Trp Gly Ser Phe Gln Asn Thr Thr Gln Phe Asn Gly Ser Met
 260 265 270
 Leu Thr Glu Asp Arg Lys Ala Gly Val Met Val Phe Gly Gln His Asn
 40 275 280 285
 Tyr Arg Pro Gly Gln Asp Ile Asp Gly Asp Asn Phe Thr Glu Leu Pro
 290 295 300
 Asn Leu Arg Asn Arg Ser Leu Gly Phe Arg Ser Tyr Tyr Lys Thr Gly
 305 310 315 320
 45 Leu Tyr Ser Lys Ala Thr Leu Glu Tyr His Ser Met Gln Glu Tyr Arg
 325 330 335
 Arg Gly Gly Asp Arg Leu Asp Asn Pro Pro Phe Glu Ala Gln Ile Ala
 340 345 350
 Glu Tyr Leu Gln His Tyr Ile Asn Gly Gly Ser Phe Lys Phe Asp Gln
 50 355 360 365
 Gly Phe Ser Gly Gly Lys Asp Phe Phe Ser Leu Tyr Ala Ser Ala Gln
 370 375 380
 Asp Val Gln Arg Arg Ser Tyr Tyr Gly Gly Asp Tyr Thr Glu Asn
 385 390 395 400
 55 Leu Leu Asn Gly Ala Val Gln Ser Gly Ser Thr Glu Ser Asp Glu Tyr
 405 410 415
 Asn Asp Ala Phe Thr Ala Leu Thr Ser Tyr Gly Thr Thr Lys Gly Phe
 420 425 430
 60 Asp Leu Gln Gly Gly Met Tyr Arg His Thr Phe Gly Glu Asn Trp
 435 440 445

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

5

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...891

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:51

	Met	Tyr	Lys	Lys	Ile	Ile	Ala	Val	Ala	Ala	Leu	Phe	Cys	Ala	Ser	Ile
1					5				10						15	
	Gly	Ile	Leu	Lys	Gly	Gln	Ser	Ser	Asp	Leu	Thr	Pro	Gln	Asp	Thr	Ile
15					20				25						30	
	Tyr	Ser	Pro	Glu	Ile	Ser	Tyr	Ala	Lys	Pro	Ile	His	Lys	Thr	Ile	Ala
					35				40					45		
	Ser	Ile	Glu	Ile	Glu	Gly	Met	Arg	Ser	Phe	Asp	Asp	Phe	Val	Leu	Arg
20					50				55					60		
	Asn	Leu	Ser	Gly	Leu	Ala	Val	Gly	Asp	Glu	Val	Leu	Ile	Pro	Gly	Asp
25					65				70					75		80
	Ala	Met	Ser	Ala	Ala	Val	Asn	Arg	Ile	Met	Arg	Gln	Gly	Tyr	Phe	Ser
					85				90					95		
	Asn	Val	Arg	Ile	Ile	Ala	Asp	Lys	Tyr	Val	Gly	Asn	Lys	Val	Tyr	Leu
30					100				105					110		
	Lys	Ile	Ile	Val	Thr	Glu	Arg	Pro	Arg	Ile	Ser	Lys	Val	Thr	Phe	Ser
					115				120					125		
	Gly	Val	Lys	Lys	Ser	Glu	Arg	Glu	Asp	Leu	Glu	Met	Lys	Ile	Gly	Leu
35					130				135					140		
	Arg	Glu	Gly	Ile	Gln	Met	Thr	Arg	Asn	Asn	Glu	Asp	Lys	Val	Arg	Gln
40					145				150					155		160
	Ile	Val	Gln	Lys	Tyr	Phe	Ser	Glu	Lys	Gly	Tyr	Arg	Asp	Ala	Ser	Ile
					165				170					175		
	Arg	Ile	Thr	Gln	Glu	Pro	Asp	Leu	Ser	Lys	Asp	Gly	Phe	Val	Asn	Val
45					180				185					190		
	Leu	Ile	Ser	Ile	Glu	Lys	Lys	Ser	Lys	Thr	Lys	Val	Asn	Glu	Ile	Tyr
					195				200					205		
	Phe	Ser	Gly	Asn	Lys	Ala	Leu	Ser	Asn	His	Lys	Leu	Arg	Met	Ala	Met
50					210				215					220		
	Lys	Asn	Thr	Asn	Ala	Lys	Phe	Ser	Leu	Arg	Lys	His	Ile	Arg	Ser	Ser
					225				230					235		240
	Phe	Leu	Lys	Leu	Phe	Ser	Thr	His	Lys	Phe	Val	Glu	Glu	Ser	Tyr	Arg
55					245				250					255		
	Glu	Asp	Leu	Val	Arg	Leu	Ile	Glu	Lys	Tyr	Gln	Glu	Tyr	Gly	Tyr	Arg
					260				265					270		
	Asp	Ala	Glu	Ile	Leu	Thr	Asp	Ser	Val	Val	Lys	Ala	Pro	Asp	Gly	Lys
60					275				280					285		
	Arg	Val	Asp	Ile	Tyr	Leu	Asn	Ile	Glu	Glu	Gly	Gln	Lys	Tyr	Tyr	Ile
					290				295					300		
	Lys	Asp	Val	Asn	Phe	Val	Gly	Asn	Ser	Gln	Tyr	Pro	Ser	Glu	Tyr	Leu
					305				310					315		320
	Glu	Arg	Val	Leu	Gly	Ile	Lys	Ser	Gly	Asp	Val	Tyr	Asn	Gln	Arg	Arg
					325				330					335		
	Leu	Ala	Lys	Arg	Leu	Asn	Glu	Asp	Glu	Asp	Ala	Val	Gly	Asn	Leu	Tyr
65					340				345					350		
	Tyr	Asn	Asn	Gly	Tyr	Ile	Phe	Ala	Trp	Val	Asp	Pro	Val	Glu	Thr	Asn
					355				360					365		
	Val	Val	Gly	Asp	Ser	Val	Ser	Leu	Asp	Ile	Arg	Ile	Ala	Glu	Gly	Lys
					370				375					380		
	Gln	Ala	Asn	Ile	Asn	Lys	Val	Ile	Ile	Lys	Gly	Asn	Thr	Val	Val	Tyr

865	870	875	880
Ser Asn Val His Phe Val Leu Gly Gln Glu Phe			
885		890	

5 (2) INFORMATION FOR SEQ ID NO:52

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 170 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

- (iii) HYPOTHETICAL: YES

- 15 (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Porphyromonas gingivalis*

- 20 (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...170

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:52

25	Met Lys Arg Phe Leu Ile Leu Ile Gly Phe Ala Leu Ala Val Ala Phe			
	1	5	10	15
	Ser Gly Phe Ser Gln Lys Phe Ala Leu Val Asp Met Glu Tyr Ile Leu			
	20	25	30	
30	Arg Asn Ile Pro Asp Tyr Glu Met Met Asn Glu Gln Leu Glu Gln Val			
	35	40	45	
	Ser Lys Lys Trp Gln Asn Glu Ile Glu Ala Leu Glu Asn Glu Ala Gln			
	50	55	60	
	Ser Met Tyr Lys Lys Tyr Gln Ser Asp Leu Val Phe Leu Ser Ala Ala			
	65	70	75	80
35	Gln Lys Lys Thr Gln Glu Glu Ala Ile Val Lys Lys Glu Gln Gln Ala			
	85	90	95	
	Ser Glu Leu Lys Arg Lys Tyr Phe Gly Pro Glu Gly Glu Leu Tyr Lys			
	100	105	110	
40	Lys Arg Ser Asp Leu Met Lys Pro Ile Gln Asp Glu Ile Trp Asn Ala			
	115	120	125	
	Ile Lys Glu Ile Ala Lys Arg Asn Asn Tyr Gln Met Val Leu Asp Arg			
	130	135	140	
	Gly Thr Ser Gly Ile Ile Phe Ala Ser Pro Ser Ile Asp Ile Ser Asp			
	145	150	155	160
45	Leu Val Leu Ser Lys Met Gly Phe Ser Lys			
	165	170		

(2) INFORMATION FOR SEQ ID NO:53

- 50 (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 163 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

- 55 (ii) MOLECULE TYPE: protein

- (iii) HYPOTHETICAL: YES

- 60 (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Porphyromonas gingivalis*

Ala Thr Thr Asp Ser Ile Thr Ile Glu Phe Ser Ser Met Gly Tyr Gln
 85 90 95
 Gly Val Ser Arg Ser Phe Pro Ser Leu Thr Lys Asp Thr Arg Leu Asn
 100 105 110
 5 Val Arg Leu Ala Glu Ala Glu Met Glu Leu Ser Ser Val Thr Val Gln
 115 120 125
 Ala Thr Lys Arg Arg Leu Asn Thr Met Glu Arg Val Asn Thr Arg Asp
 130 135 140
 Leu Arg Val Asn Ala Gly Pro Thr Gly Gly Val Glu Ser Leu Ile Ser
 145 150 155 160
 10 Thr Tyr Ala Gly Val Thr Gln Asn Asn Glu Leu Ser Ser Gln Tyr Ser
 165 170 175
 Val Arg Gly Gly Ser Tyr Asp Glu Asn Met Val Tyr Val Asn Gly Val
 180 185 190
 15 Glu Val Tyr Arg Pro Leu Leu Val Arg Ser Ala Gln Gln Glu Gly Leu
 195 200 205
 Ser Phe Val Asn Pro Asp Leu Thr Gln Ser Val Gln Phe Ser Ala Gly
 210 215 220
 Gly Phe Thr Ala Asp Tyr Gly Asp Lys Met Ser Ser Val Leu Asp Ile
 225 230 235 240
 20 Arg Tyr Lys Gln Pro Gln Glu Lys Glu Gly Ala Val Leu Leu Gly Met
 245 250 255
 Leu Gln Ser Ser Ala Tyr Tyr Gly Ser Ser Ala Gly Ala Phe Ser Gln
 260 265 270
 25 Ile Thr Gly Val Arg Tyr Lys Ser Ala Lys Ser Leu Leu Gly Thr Thr
 275 280 285
 Asp Thr Lys Ala Glu Tyr Asp Pro Ile Tyr Ala Asp Gly Gln Thr Phe
 290 295 300
 Met Thr Tyr Arg Phe Ser Pro Lys Leu Ser Val Ser Phe Leu Gly Asn
 305 310 315 320
 30 Ile Ser Gln Thr Arg Tyr Lys Phe Val Pro Gln Thr Arg Glu Thr Ser
 325 330 335
 Phe Gly Thr Leu Ser Asp Ala Lys Lys Leu Lys Ile Phe Phe Asp Gly
 340 345 350
 35 Gln Glu Gln Asp Arg Phe Leu Thr Tyr Phe Gly Ala Phe Ser Met Asn
 355 360 365
 Phe Val Pro Asp Asp Lys Gln Arg His Thr Val Thr Leu Ser Ala Phe
 370 375 380
 Asn Ser Asn Glu Arg Glu Thr Tyr Asp Ile Gln Gly Glu Tyr Phe Leu
 385 390 395 400
 40 Asn Asp Val Gln Leu Gly Ala Asp Gly Thr Ala Ser Met Ala Ser Gly
 405 410 415
 Ser Glu Asn Ser Asn Gly Leu Gly Ile Gly Arg Asn His Glu His Ala
 420 425 430
 45 Arg Asn Arg Leu Ser Tyr Arg Val Leu Asn Met Gly Tyr Arg Gly Glu
 435 440 445
 Met Lys Leu Asn Glu Lys His Arg Leu Gln Ala Gly Val Ser Ala Gln
 450 455 460
 Met Glu Lys Ile Ala Asp His Ile Ser Glu Trp Glu Arg Arg Asp Ser
 465 470 475 480
 50 Val Gly Tyr Asn Leu Pro His Ser Glu Thr Val Leu Leu Met Tyr Asn
 485 490 495
 Asn Leu Tyr Ala Asp Thr Gln Met Arg Gly Thr Arg Leu Ser Ala Phe
 500 505 510
 55 Val Gln Asp Arg Phe Asn Phe Ser Met Gly Gly Thr Phe Ser Leu
 515 520 525
 Ile Pro Gly Ile Arg Ala Ser Trp Trp Ser Phe Asn Lys Glu Leu Leu
 530 535 540
 60 Val Ser Pro Arg Ile Ser Val Gly Tyr Ser Pro Glu Ser Asn Pro Ala
 545 550 555 560

	35	40	45
	Glu Gln Ala Gly Val Asn Thr Lys Pro Tyr Asn Pro Gly Tyr Ala Thr		
	50 55	60	
5	Asn Asn Ile Gly Leu Phe Gly Gln Ala Asn Phe Tyr Leu Leu Asn Asp		
	65 70	75	80
	Ala Leu Ser Ile Ser Ala Gly Ala Arg Ala Asp Phe Met Phe Asp		
	85 90	95	
	Leu Lys Ala Asn Glu Tyr Leu Asn Asn Glu Ala Lys Gln Glu Thr His		
	100 105	110	
10	Asn Val Ile Asn Pro Asn Val Gly Ile Lys Tyr Glu Phe Val Lys Gly		
	115 120	125	
	Leu Thr Ala His Gly Thr Phe Gly Ser Ala Phe Ser Ala Pro Asp Ala		
	130 135	140	
15	Phe Gln Lys Ala Gly Gln Tyr Val Gly Pro Phe Gly Thr Thr Ile Gly		
	145 150	155	160
	Asn Pro Asp Leu Lys Pro Glu Lys Ser Met Thr Trp Asp Phe Gly Ile		
	165 170	175	
	Gly Tyr Ser Asn Ala Arg Cys Gly Ile Gln Ala Asp Val Thr Leu Thr		
	180 185	190	
20	Tyr Phe His Thr Asp His Lys Asp Leu Ile Leu Ser Ser Pro Asp Tyr		
	195 200	205	
	Ala Asn Asn Ile Thr Thr Tyr Ile Asn Ala Asp Lys Ala Arg Met Ser		
	210 215	220	
25	Gly Ile Glu Ala Leu Leu Ser Tyr Asp Phe Gly Ser Leu Phe Ala Asn		
	225 230	235	240
	Lys Phe Ser Leu Arg Ala Phe Ala Asn Ala Thr Ile Met Leu Asn Ser		
	245 250	255	
	Glu Met Lys Lys Ser Gln Thr Asp Ala Pro Trp Ser Glu Met Tyr Tyr		
	260 265	270	
30	Val Arg Lys Gln Asn Ile Thr Phe Gly Ile Glu Tyr Arg Gly Lys Glu		
	275 280	285	
	Gly Leu Glu Val Met Leu Asn Gly Arg Phe Met Gly Arg Arg Ile Glu		
	290 295	300	
35	Gln Asn Trp Tyr Ala Tyr Tyr Pro Glu Val Arg Pro Glu Leu Gln Gln		
	305 310	315	320
	Leu Leu Ala Ala Glu Glu Pro Glu Leu Ala Ala Gln Gly Leu Leu Arg		
	325 330	335	
	: His Pro Gln Ala Met Val Phe Asn Ala Ser Ala Tyr Tyr His Met Asn		
	340 345	350	
40	Lys Tyr Leu Thr Phe Gly Val Asn Leu Asn Asn Ile Leu Asp Glu Leu		
	355 360	365	
	Tyr Thr Glu Lys Asp Gly Tyr His Met Pro Gly Arg Asn Ile Met Gly		
	370 375	380	
45	Lys Val Met Val Asn Phe		
	385 390		

(2) INFORMATION FOR SEQ ID NO:56

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 462 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

55 (ii) MOLECULE TYPE: protein

55 (iii) HYPOTHETICAL: YES

60 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Porphyromonas gingivalis*

Ala Arg Leu Asn Tyr Asn Gln Ala Ile Phe Asp Phe Met Thr Ala Lys
 435 440 445
 Ala Glu Leu Asp Lys Met Asn Gly Met Gly Ile Pro Glu Gln
 450 455 460

5

(2) INFORMATION FOR SEQ ID NO:57

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 526 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: protein

15 (iii) HYPOTHETICAL: YES

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Porphyromonas gingivalis*

25 (ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...526

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57

25 Met Ala Asn Asn Thr Leu Leu Ala Lys Thr Arg Arg Tyr Val Cys Leu
 1 5 10 15
 Val Gly Phe Cys Trp Leu Met Ala Met Met His Leu Ser Gly Gln Glu
 20 25 30
 30 Val Thr Met Trp Gly Asp Ser His Gly Val Ala Pro Asn Gln Val Arg
 35 40 45
 Arg Thr Leu Val Lys Val Ala Leu Ser Glu Ser Leu Pro Pro Gly Ala
 50 55 60
 Lys Gln Ile Arg Ile Gly Phe Ser Leu Pro Lys Glu Thr Glu Glu Lys
 35 65 70 75 80
 40 Val Thr Ala Leu Tyr Leu Leu Val Ser Asp Ser Leu Ala Val Arg Asp
 85 90 95
 Leu Pro Asp Tyr Lys Gly Arg Val Ser Tyr Asp Ser Phe Pro Ile Ser
 100 105 110
 45 Lys Glu Asp Arg Thr Thr Ala Leu Ser Ala Asp Ser Val Ala Gly Arg
 115 120 125
 Arg Phe Phe Tyr Leu Ala Ala Asp Ile Gly Pro Val Ala Ser Phe Ser
 130 135 140
 Arg Ser Asp Thr Leu Thr Ala Arg Val Glu Glu Val Ala Val Asp Gly
 145 150 155 160
 50 Arg Pro Leu Pro Leu Lys Glu Leu Ser Pro Ala Ser Arg Arg Leu Tyr
 165 170 175
 Arg Gly Tyr Glu Ala Leu Phe Val Pro Gly Asp Gly Gly Ser Arg Asn
 180 185 190
 Tyr Arg Ile Pro Ala Ile Leu Lys Thr Ala Asn Gly Thr Leu Ile Ala
 195 200 205
 Met Ala Asp Arg Arg Lys Tyr Asn Gln Thr Asp Leu Pro Glu Asp Ile
 210 215 220
 Asp Ile Val Met Arg Arg Ser Thr Asp Gly Gly Lys Ser Trp Ser Asp
 225 230 235 240
 55 Pro Arg Ile Ile Val Gln Gly Glu Gly Arg Asn His Gly Phe Gly Asp
 245 250 255
 Val Ala Leu Val Gln Thr Gln Ala Gly Lys Leu Leu Met Ile Phe Val
 260 265 270
 60 Gly Gly Val Gly Leu Trp Gln Ser Thr Pro Asp Arg Pro Gln Arg Thr

Leu Glu Ser Ala Tyr Lys Ala Leu Lys Glu Lys Gln Ile Leu Val Ala
 65 70 75 80
 Asp Tyr Leu Lys Asn Lys Gln Leu Pro Asp Ser Ser Tyr Ile Phe Ser
 85 90 95
 5 Ser Val Ala Ile Ser Lys Glu Tyr Asn Tyr Tyr Asp Pro Arg Gln
 100 105 110
 Glu Gln Asn Val Arg Thr Phe Ala Gly Tyr Leu Leu Ser Gln Thr Val
 115 120 125
 Thr Val Thr Ser Gln Asp Ile Glu His Val Glu Lys Ile Ser Arg Asp
 10 130 135 140
 Ile Thr Glu Leu Ile Asn Gln Gly Val Glu Ile Thr Ser Asp Arg Pro
 145 150 155 160
 Ala Tyr Tyr Tyr Thr Lys Leu Asn Asp Leu Lys Val Glu Met Leu Arg
 165 170 175
 15 Asn Ala Ser Glu Asp Ala Phe Asn Arg Ala Ser Val Ile Ala Glu Gly
 180 185 190
 Ser Gly Ser Ser Val Gly Lys Met Leu Ser Ser Met Gly Val Phe
 195 200 205
 Gln Ile Val Gly Leu Asn Ser Asn Glu Asp Tyr Ser Trp Gly Gly Ser
 20 210 215 220
 Phe Asn Thr Ser Ser Lys Met Lys Thr Ala Ser Ile Thr Val Lys Ala
 225 230 235 240
 Ser Phe Ala Leu Lys
 245
 25

(2) INFORMATION FOR SEQ ID NO:59

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 276 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- 35 (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Porphyromonas gingivalis*
- 40 (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...276
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:59

45 Met Lys Lys Thr Ile Ala Ile Ile Ala Ser Ala Leu Leu Ala Leu Gly
 1 5 10 15
 Ala Val Gly Cys Lys Lys Asn Ala Asp Thr Thr Ala Val Ser Glu Lys
 20 25 30
 50 Asp Ser Ile Ala Leu Ser Met Gly Ile Leu Tyr Gly Gln Asp Phe Ala
 35 40 45
 Asn Gln Phe Glu Met Ser Arg Leu Gln Gly Gln Pro Ile Asp Ser Val
 50 55 60
 Ala Phe Leu Asp Gly Phe Lys Tyr Gly Ile Asp Thr Thr Arg Phe Ser
 65 70 75 80
 55 Tyr Asn Leu Gly Ala Ile Tyr Ala Ser Asn Ile Ala Arg Gln Leu Ala
 85 90 95
 His Asp Ser Ile Asp Ile Asp Lys Phe Tyr Ala Ala Met Arg Ala Ala
 100 105 110
 60 Leu Leu Lys Asp Thr Val Ser Ile Ala Met Lys Pro Ala Asp Ala Gln

Leu Lys Lys Asp Ser Leu Lys Ala Lys Ile Ser Tyr Thr Val Asp Met
 145 150 155 160
 Ala Ser Pro Tyr His Tyr Asp Ser Ile Ile Pro Leu Pro Ile Ser Thr
 165 170 175
 5 Phe Pro Asp Ser Ile Leu Ala Tyr Arg Gln Thr Pro Ser Leu Ile Arg
 180 185 190
 Lys Gly Asp Gln Phe Asn Leu Ala Lys Leu His Glu Glu Arg Gln Thr
 195 200 205
 Ile Ser Ala Leu Leu Arg Asp Asn Gly Tyr Tyr Phe Arg Pro Gln
 10 210 215 220
 Asp Ile Ile Tyr Glu Ala Asp Thr Leu Leu Val Arg Gly Ala Val Cys
 225 230 235 240
 Leu Arg Ala Lys Leu Ser Glu Asp Thr Pro Pro Gln Ala Met Arg Pro
 245 250 255
 15 Trp Arg Ile Gly Lys Arg Thr Ala Val Leu Leu Gly Met Asn Gly Glu
 260 265 270
 Ser Pro Thr Asp Ser Leu Glu Val Glu Asp Met Lys Val Leu Tyr Tyr
 275 280 285
 Arg Lys Met Pro Val Arg Pro Lys Ile Leu Ala Lys Arg Phe Arg Phe
 20 290 295 300
 Phe Ser Gly Asn Leu Tyr Arg Gln Lys Asp Asp Glu Thr Thr Arg Lys
 305 310 315 320
 Ser Leu Ala Arg Leu Gly Ala Phe Ser Val Ile Asp Leu Asn Phe Leu
 325 330 335
 25 Gln Arg Asp Ser Ile Ser Gly Leu Leu Asp Val Arg Leu Leu Thr Thr
 340 345 350
 Leu Asp Lys Pro Trp Asp Ala Ser Leu Glu Thr Leu Phe Thr Ser Lys
 355 360 365
 Ser Asn Asp Phe Ile Gly Pro Gly Leu Asn Phe Ala Leu Ala Arg Arg
 30 370 375 380
 Asn Val Phe Gly Gly Glu Asn Leu Ser Trp Asn Ile Gly Gly Ser
 385 390 395 400
 Tyr Glu Trp Glu Thr Gly Asn Arg Pro Glu Asn Ser Ser Asn Arg Leu
 405 410 415
 35 Ile Asp Ile Asn Ser Tyr Asn Met Asn Thr Ala Val Asn Leu Ser Phe
 420 425 430
 Pro Ser Ile Val Phe Pro Gly Leu Leu Asp Lys Tyr Tyr Tyr Pro
 435 440 445
 Thr Thr Thr Phe Gln Ala Ser Ala Thr Ala Leu Asn Arg Ala His
 40 450 455 460
 Tyr Phe Ser Met Tyr Ser Phe Gly Phe Ser Thr Thr Tyr Glu Phe Gln
 465 470 475 480
 Pro Ser Lys Glu His Arg His Ala Ile Phe Pro Leu Lys Leu Asn Tyr
 485 490 495
 45 Asn Leu Leu Gly His Gln Thr Glu Thr Phe Gln Ala Ile Thr Ala Asn
 500 505 510
 Asn Pro Pro Leu Leu Leu Ser Leu Gln Ser Gln Phe Leu Ala Gln Met
 515 520 525
 50 Gly Tyr Ile Tyr Thr Phe Asn Lys Ser Val Ser Glu Lys Ser Pro His
 530 535 540
 His Leu Trp Met Gln Phe Gly Leu Ser Glu Ala Gly Asn Leu Leu Asn
 545 550 555 560
 Leu Ile Tyr Leu Ala Ala Gly Lys Lys Tyr Ser Asp Thr Lys Asn Phe
 565 570 575
 55 Val Gly Val Pro Phe Ser Gln Phe Ile Lys Ala Thr Gly Glu Leu Arg
 580 585 590
 Tyr Ser Tyr Thr Ile Asp Arg Asn Gln Ser Leu Ala Thr Arg Phe Gly
 595 600 605
 Thr Gly Val Ile Tyr Ser Tyr Gly Asn Met Arg Val Ala Pro Tyr Ser
 60 610 615 620

	145	150	155	160
	Asp Val Lys Asn Pro Leu Leu Pro Pro Val Ala Leu Gly Asn Ser Leu			
	165	170	175	
5	Pro Ser Ala Tyr Lys Val Gly Ile Ser Glu Gly Ser Pro Leu Ser Pro			
	180	185	190	
	Ile Val Leu Asp Glu Glu Arg Lys Ala Ile Ala Arg His Met Arg Asn			
	195	200	205	
	Asn Gly Phe Trp Lys Phe Ser Ala Glu Asp Val Tyr Tyr Glu Ala Asp			
10	210	215	220	
	Thr Thr Val Ser Gly Gly Ser Gly Thr Lys Ser Ala Asp Leu Lys Leu			
	225	230	235	240
	Val Val Asn Gly Ile Gly Arg Tyr Pro Tyr Arg Ile Gly Arg Val Phe			
	245	250	255	
15	Phe His Ala Asp Tyr Asp Pro Leu Glu Ser Asp Phe Arg Val Gln Glu			
	260	265	270	
	Leu Pro Arg Ile Asp Ser Ile Ser Arg Gly Asp Tyr Thr Val Tyr Tyr			
	275	280	285	
	Gly Ser Arg Gly Arg Tyr Ile Arg Ala Ser Ala Leu Thr Arg Ser Val			
20	290	295	300	
	Ser Val Thr Pro Gly Ala Phe Phe Cys Glu Asp Asp Val Glu Arg Ser			
	305	310	315	320
	Tyr Ile Lys Leu Asn Ala Leu Pro Ile Val Arg Asn Val Asn Ile Arg			
	325	330	335	
25	Phe Val Glu His Asn Gly Lys Asp Glu Ile Ala Leu Ala Asp Ser Ser			
	340	345	350	
	Arg Leu Val Asp Cys Tyr Ile Leu Thr Val Pro Ala Lys Ser Lys Ser			
	355	360	365	
	Phe Glu Ala Glu Val Leu Gly Thr Asn Ser Ala Gly Asp Phe Gly Ala			
	370	375	380	
30	Ala Leu Ser Leu Gly Phe Thr Asp Arg Asn Leu Phe Arg Gly Ala Glu			
	385	390	395	400
	Met Phe Asn Ile Lys Leu Lys Gly Ala Tyr Glu Ala Ile Arg Lys Gly			
	405	410	415	
35	Ser His Ser Phe Met Glu Tyr Gly Val Glu Ser Ser Leu Arg Phe Pro			
	420	425	430	
	Arg Leu Leu Phe Pro Phe Ile Ser Asp Glu Thr Arg Arg Arg Leu Arg			
	435	440	445	
	Ala Ser Thr Glu Trp Lys Ile Gly Tyr Asn Tyr Gln Thr Arg Pro Glu			
	450	455	460	
40	Phe Asp Arg Val Ile Leu Ser Ala Gln Leu Asn Tyr Ser Trp Gln Thr			
	465	470	475	480
	Tyr Leu His Asn Arg Leu Arg His Thr Ile Arg Leu Leu Asp Val Asp			
	485	490	495	
45	Tyr Leu His Leu Pro Tyr Ile Asp Pro Asp Phe Ala Gln Ser Leu Pro			
	500	505	510	
	Pro Thr Thr Ala Leu Tyr Asn Tyr Thr Glu Gln Phe Ile Leu Gly Ser			
	515	520	525	
	Ala Tyr Ile Leu Asn Tyr Thr Thr Ala Ser Ser Met Glu Arg Thr Val			
	530	535	540	
50	Ser Asn Pro Phe Thr Ala Arg Phe Ser Ile Gln Thr Ala Gly Asn Leu			
	545	550	555	560
	Leu Gln Ala Ile Ser Tyr Leu Thr Asp Ser Pro Lys Asp Glu His Gly			
	565	570	575	
55	Leu Tyr Lys Met Phe Gly Leu His Tyr Ala Gln Phe Val Lys Leu Asp			
	580	585	590	
	Leu Asp Leu Ala Lys Thr Val Leu Leu Glu Lys Asp Asn Thr Leu Ala			
	595	600	605	
	Leu His Leu Gly Phe Gly Leu Ala Phe Pro Tyr Gly Asn Ala Arg His			
	610	615	620	
60	Ile Pro Phe Glu Leu Arg Tyr Phe Ala Gly Ser Asn Ser Val Arg			

Gly Ser Gly Gly Phe Gly Asp Gly Arg Thr Asn Val Arg Gly Phe Asp
 165 170 175
 Thr Tyr Asn Phe Gly Val Leu Ile Asn Gly Val Pro Val Asn Gly Met
 180 185 190
 5 Glu Asp Gly Lys Val Tyr Trp Ser Asn Trp Ser Gly Leu Met Asn Gln
 195 200 205
 Ala Ser Thr Ile Gln Ile Gln Arg Gly Leu Gly Ala Ser Lys Leu Gly
 210 215 220
 Ile Ser Ser Val Gly Gly Thr Met Asn Ile Ile Thr Lys Thr Thr Asp
 10 225 230 235 240
 Ala Asn Thr Gly Gly Ser Ala Tyr Val Gly Met Gly Asn Asp Gly Leu
 245 250 255
 His Lys Glu Ser Phe Ser Ile Ser Thr Gly Met Asn Asp Gly Trp Ala
 260 265 270
 15 Ile Thr Ile Ala Gly Ser His Met Thr Gly Leu Gly Tyr Val Lys Gly
 275 280 285
 Leu Lys Gly Arg Ala Phe Ser Tyr Phe Phe Asn Val Ser Lys Lys Phe
 290 295 300
 Asn Glu Arg His Thr Leu Ser Leu Thr Gly Phe Gly Ala Pro Gln Trp
 20 305 310 315 320
 His Asn Gln Arg Ser Ser Lys Tyr Ser Val Ala Asp Tyr Asp Lys Tyr
 325 330 335
 Gly Ile Arg His Asn Gln Ser Phe Gly Tyr Leu Arg Gly Glu Leu Thr
 340 345 350
 25 Pro Thr Ala Tyr Ala Tyr Asn Thr Tyr His Lys Pro Gln Phe Ser Leu
 355 360 365
 Asn His Phe Trp Lys Met Asp Glu Asn Thr Ser Leu Tyr Thr Ala Unk
 370 375 380
 Tyr Ala Ser Leu Ala Thr Gly Gly Arg Arg Ala Tyr Gly Lys Asn
 30 385 390 395 400
 Ser Lys Trp Val Leu Ile Asn Tyr Asn Thr Gly Gln Pro Tyr Glu Gln
 405 410 415
 Thr Lys Val Thr Pro Asp Gly Leu Ile Asp Tyr Asp Ala Val Leu Ala
 420 425 430
 35 Ala Asn Ala Ala Ser Asn Gly Ser Glu Ala Ile Phe Ala Leu Gly
 435 440 445
 Ser Asn Ser His Lys Trp Phe Gly Leu Leu Ser Ser Phe Lys Lys Lys
 450 455 460
 Leu Asn Ser Ser Leu Thr Leu Thr Ala Gly Tyr Asp Gly Arg Tyr Tyr
 40 465 470 475 480
 Arg Gly Asp His Tyr Asp Lys Ile Thr Asp Leu Leu Gly Gly Ser Tyr
 485 490 495
 Tyr Ile Glu Asp Pro Lys Thr Lys Leu Ala Tyr His Ala Glu Gly Gln
 500 505 510
 45 Gln Leu Lys Val Gly Asp Ile Val Asn Arg Asp Tyr Thr Gly Glu Ile
 515 520 525
 Met Trp His Gly Leu Phe Ala Gln Met Glu His Ser Ser Glu Trp Ile
 530 535 540
 Asp Ala Phe Val Ser Gly Ser Ile Asn Tyr Glu Leu Tyr Arg Asn His
 50 545 550 555 560
 Asn Tyr Gly Gly Ser Lys Ser Thr Gly Tyr Leu Pro Gly Val Ser Pro
 565 570 575
 Trp Lys Ser Phe Leu Pro Trp Ser Gly Lys Ala Gly Leu Ser Tyr Lys
 580 585 590
 55 Phe Ala Gln Gly His Asn Val Phe Ala Asn Gly Gly Phe Phe Thr Arg
 595 600 605
 Ala Pro Leu Phe Gly Asn Ile Tyr Ala Ala Gly Ala Ile Ile Pro Asn
 610 615 620
 Asp Lys Ala Asn Met Glu Lys Val Leu Thr Gly Glu Val Gly Tyr Gly
 60 625 630 635 640

	65	70	75	80
	Leu Leu Asp Asn Glu Val Lys Glu Leu Gln Ser Asp Ile Asp Ser Met			
	85	90	95	
5	Thr Gly Val Cys His Gln Leu Ser Val Glu Glu Lys Ala Arg Ser Asp			
	100	105	110	
	Glu Tyr Ala Gln Ala Leu Gln Ser Met Gln Lys Arg Lys Arg Ser Leu			
	115	120	125	
	Asp Arg Ile Leu Phe Ile Ser Ser Ala Lys Ser Phe Asp Glu Gly Met			
	130	135	140	
10	Arg Arg Met Arg Phe Leu Glu Gln Tyr Ala Ser Ala Tyr Lys Leu Ala			
	145	150	155	160
	Ser Val Arg Leu Arg Asp Thr Arg Ser Lys Leu Glu Thr Glu Arg Ala			
	165	170	175	
15	Thr Val Glu Asp Ala Lys Lys Glu Lys Gly His Leu Leu Val Ile Arg			
	180	185	190	
	Glu Glu Glu Lys Lys Leu Glu Gly Gln Gln Ala Glu Gln Arg Arg			
	195	200	205	
	Gln Val Gln Ala Leu Gly Ala Lys Gln Lys Asp Leu Glu Ala Gln Leu			
	210	215	220	
20	Arg Lys Gln Lys Lys Gln Ala Glu Ala Leu Asn Arg Lys Ile Glu Lys			
	225	230	235	240
	Gln Ile Ala Lys Glu Ile Glu Ala Ala Glu Arg Arg Ala Arg Glu Glu			
	245	250	255	
25	Arg Glu Arg Leu Ala Arg Glu Ala Lys Ala Lys Gly Lys Pro Val Pro			
	260	265	270	
	Ala Glu Pro Glu Arg Lys Ala Glu Thr Lys Gly Gly Tyr Ala Met Asp			
	275	280	285	
	Ala Ser Glu Arg Ala Leu Ser Gly Ser Phe Ala Gln Asn Lys Gly Arg			
	290	295	300	
30	Leu Pro Gly Pro Val Arg Gly Arg Tyr Arg Ile Val Ser Asp Phe Gly			
	305	310	315	320
	Val His Gln His Ser Glu Leu Lys Lys Val Gln Val Asn Asn Gly Gly			
	325	330	335	
	Ile Asp Ile Ala Val Ala Thr Gly Ser Asp Ala Thr Ser Val Phe Asp			
35	340	345	350	
	Gly Val Val Ser Ser Val Phe Val Ile Pro Gly Tyr Asn Ser Ala Val			
	355	360	365	
	Met Val Arg His Gly Asn Tyr Ile Thr Val Tyr Ala Asn Leu Ser Lys			
	370	375	380	
40	Val Tyr Val Asn Ser Gly Thr Arg Val Lys Thr Gly Gln Ala Leu Gly			
	385	390	395	400
	Arg Ala Tyr Thr Asp Pro Ser Asn Asn Gln Thr Ile Ile His Phe Glu			
	405	410	415	
45	Ile Trp Lys Glu Arg Ser Lys Gln Asn Pro Arg Leu Trp Leu Arg			
	420	425	430	

(2) INFORMATION FOR SEQ ID NO:64

50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

55 (ii) MOLECULE TYPE: protein

 (iii) HYPOTHETICAL: YES

60 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Porphyromonas gingivalis*

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Porphyromonas gingivalis*

5 (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...848

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65

10	Met Ile Gly Lys Lys Ile Phe Phe Ile Leu Leu Ala Leu Ile Ala Phe		
	1 5 10 15		
	Ser Gly Leu Asn Ala Ala Thr Asp Thr Glu Phe Lys Tyr Pro Thr Asp		
	20 25 30		
15	Ala Asn Ile Ile Gly His Val Lys Asp Ser Lys Thr Gly Glu His Leu		
	35 40 45		
	Val Gly Ile Thr Ile Ala Ile Lys Gly Thr Thr Phe Gly Thr Ser Thr		
	50 55 60		
	Asp Ala Thr Gly His Tyr Tyr Leu Arg Asn Leu Arg Pro Gly Glu Ile		
	65 70 75 80		
20	Thr Leu Ile Met Arg Gly Met Gly Tyr Lys Ser Gln Glu Arg Val Val		
	85 90 95		
	Arg Val Glu Lys Asp Lys Thr Ile Glu Val Asn Phe Glu Ala Glu Glu		
	100 105 110		
	Asp Ala Ile Asn Leu Asp Glu Val Val Ile Ser Ala Asn Arg Glu Leu		
25	115 120 125		
	Thr Leu Arg Arg Leu Ala Pro Thr Leu Val Asn Val Leu Asn Glu Lys		
	130 135 140		
	Val Phe Ser Gln Val Asn Ala Ser Asn Leu Ala Gln Gly Leu Ser Phe		
	145 150 155 160		
30	Gln Pro Gly Val Arg Val Glu Asn Asn Cys Gln Asn Cys Gly Phe Asn		
	165 170 175		
	Gln Val Arg Ile Asn Gly Leu Asp Gly Arg Tyr Ala Gln Ile Leu Ile		
	180 185 190		
	Asp Ser Arg Pro Ile Met Ser Ala Leu Ala Gly Val Tyr Gly Leu Glu		
35	195 200 205		
	Gln Ile Pro Ala Asn Met Ile Glu Arg Val Glu Val Val Arg Gly Gly		
	210 215 220		
	Gly Ser Ala Leu Tyr Gly Ser Ser Ala Ile Ala Gly Val Val Asn Ile		
	225 230 235 240		
40	Ile Thr Lys Glu Pro Ser His Asn Ser Phe Thr Phe Asn Glu Ser Leu		
	245 250 255		
	Ser Phe Thr Gly Phe Ser Lys Leu Asp Asn Asn Thr Asn Phe Asn Ala		
	260 265 270		
	Ser Ile Val Ser Asp Asp Asn Arg Ala Gly Ala Met Val Phe Gly Gln		
45	275 280 285		
	Ala Arg Tyr Arg Asn His Trp Asp Ala Asn Asn Asp Gly Tyr Ser Glu		
	290 295 300		
	Leu Gly Lys Ile Asp Ala Arg Ser Leu Gly Ala His Ser Tyr Leu Arg		
	305 310 315 320		
50	Leu Ser Asp Tyr Ser Lys Leu Thr Gly Glu Phe His Thr Ile Ser Glu		
	325 330 335		
	Phe Arg Arg Gly Gly Asp Arg Ile Asp Leu Pro Pro His Val Val Gly		
	340 345 350		
	Val Ala Glu Gln Thr Asp His Ser Val Phe Ser Gly Asn Leu Lys Tyr		
55	355 360 365		
	Asp Leu Phe Ser Ser Asn Tyr Lys His His Phe Gln Ala Tyr Thr Ser		
	370 375 380		
	Gly Gln Ile Val Asn Arg Lys Ser Tyr Tyr Gly Gly Ile Gly Glu Ile		
	385 390 395 400		
60	Asp Val Asn Gly His Pro Gly Gly Thr Glu Gly Tyr Pro Ile Pro Gln		

- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

5 (iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

10 (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...202

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66